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OM protein - protein search, using sw model

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Run on:     January  5, 2006, 13:48:12 ; Search time 27 Seconds
                                          (without alignments)
                                  1831.113 Million cell updates/sec

Title:           US-09-943-780-69
Perfect score:   3135
Sequence:        1 MCSRVPLLPLLLLALGPG..........PLMGFPGPGLQSPLHAKPYI 598

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        572060 seqs, 8675679 residues

Total number of hits satisfying chosen parameters:     572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :       Issued_Patents AA:*
            1: /cgn2_6/ptcdata/1/iaa/5_COMB.pep:*
            2: /cgn2_6/ptcdata/1/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
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Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	3135	100.0	598	2	US-09-866-028-69	Sequence 69, Appl
2	3135	100.0	598	2	US-09-944-457-69	Sequence 69, Appl
3	3135	100.0	598	2	US-09-945-584-69	Sequence 69, Appl
4	3135	100.0	598	2	US-09-944-944-69	Sequence 69, Appl
5	3135	100.0	598	2	US-09-945-587-69	Sequence 69, Appl
6	3083.5	98.4	673	2	US-09-063-950-2	Sequence 2, Appli
7	3083.5	98.4	673	2	US-09-991-181-52	Sequence 52, Appl
8	3083.5	98.4	673	2	US-09-990-444-52	Sequence 52, Appl
9	3083.5	98.4	673	2	US-09-997-333-52	Sequence 52, Appl
10	3083.5	98.4	673	2	US-09-992-598-52	Sequence 52, Appl
11	337	10.7	653	2	US-09-520-781-10	Sequence 10, Appl
12	337	10.7	653	2	US-09-957-187-10	Sequence 10, Appl
13	337	10.7	653	2	US-09-991-053-10	Sequence 10, Appl
14	333	10.6	590	2	US-09-520-781-12	Sequence 12, Appl
15	333	10.6	590	2	US-09-957-187-12	Sequence 12, Appl
16	333	10.5	653	2	US-09-991-053-12	Sequence 12, Appl
17	330	10.5	653	2	US-09-991-181-229	Sequence 229, Appl
18	330	10.5	653	2	US-09-990-444-229	Sequence 229, App
19	330	10.5	653	2	US-09-997-333-229	Sequence 229, App
20	330	10.5	653	2	US-09-992-598-229	Sequence 229, App
21	322	10.3	605	2	US-09-063-950-5	Sequence 5, Appli
22	320	10.2	660	2	US-09-907-794A-28	Sequence 28, Appl
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47	302	9.6	605	2	US-08-487-072A-49	Sequence 49, Appl
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95	271	8.6	473	2	US-10-020-445A-400	Sequence 400, App
96	259	8.3	610	1	US-07-821-717B-6	Sequence 6, Appli
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116	252	8.0	566	2	US-09-191-647-12	Sequence 12, App
117	252	8.0	567	2	US-10-037-417-105	Sequence 105, App
118	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appli
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120	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appli
121	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, Ap
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193	Sequence 29, Appl	US-09-964-956-29	2	440	6.6	207.5
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238	Sequence 4, Appli	PCT-US91-09055-4	4	224	6.2	193.5
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241	Sequence 290, App	US-09-905-125A-290	2	1059	6.1	190
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258	190	6.1	1119	US-09-904-920A-294	Sequence 294, App
259	190	6.1	1119	US-09-909-064-294	Sequence 294, App
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261	190	6.1	1119	US-09-906-618-294	Sequence 294, App
262	190	6.1	1119	US-09-906-646-294	Sequence 294, App
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288	178	5.7	368	US-08-458-834-3	Sequence 3, App
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389	152	4.8	786	2	US-09-949-002-351	Sequence 351, APP
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404	150	4.8	259	US-09-909-064-71	Sequence 71, Appl
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478	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appli
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529	130.5	4.2	878	2	US-09-556-706B-2	Sequence 2, Appli
530	130.5	4.2	878	2	US-09-724-418A-2	Sequence 2, Appli
531	130.5	4.2	3729	2	US-08-804-227C-4	Sequence 4, Appli
532	130	4.1	619	2	US-10-037-417-34	Sequence 34, Appl
533	130	4.1	645	2	US-10-101-464A-920	Sequence 920, App
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555	128	4.1	717	2	US-10-101-464A-810	Sequence 810, App
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557	127.5	4.1	1522	2	US-10-144-198-31	Sequence 31, Appl
558	127.5	4.1	1581	2	US-09-949-002-414	Sequence 414, App
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ALIGNMENTS

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; Patent No. 6642360
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT: Botstein, David
;  APPLICANT: Eaton, Dan
;  APPLICANT: Ferrara, Napoleone
;  APPLICANT: Filvaroff, Ellen
;  APPLICANT: Gerritsen, Mary
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Godowski, Paul
;  APPLICANT: Grimaldi, Christopher
;  APPLICANT: Gurney, Austin
;  APPLICANT: Hillan, Kenneth
;  APPLICANT: Kljavin, Ivar
;  APPLICANT: Napier, Mary
;  APPLICANT: Roy, Margaret
;  APPLICANT: Tumas, Daniel
;  APPLICANT: Wood, William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION: ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/866,028
;  CURRENT FILING DATE: 2001-05-25
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
;  LENGTH: 598
;  TYPE: PRT
;  ORGANISM: Homo Sapien
US-09-866-028-69

  Query Match       100.0%;  Score 3135;  DB 2;  Length 598;
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  Matches  598;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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RESULT 2
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; Sequence 69, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 17, 1997
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-69

Query Match   100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity   100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSOPQTVFCTAROGTTVPRDVPPDTVGLYVF 60
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Db   1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSOPQTVFCTAROGTTVPRDVPPDTVGLYVF 60
Qy   61 ENGITMLDASSFAGLPGLLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ENGITMLDASSFAGLPGLLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
Qy 121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
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Qy   121  ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL  180
Db   121  ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL  180

Qy   181  RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240
Db   181  RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240

Qy   241  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL   300
Db   241  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL   300

Qy   301  APTWLSPTAPATEAPSPPSTAPPTVGPVPQPDCPPSTCLNGGTCHLGTRHHLACLCPEG   360
Db   301  APTWLSPTAPATEAPSPPSTAPPTVGPVPQPDCPPSTCLNGGTCHLGTRHHLACLCPEG   360

Qy   361  FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR  420
Db   361  FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR  420

Qy   421  LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT  480
Db   421  LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT  480

Qy   481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540
Db   481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540

Qy   541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI   598
Db   541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI   598
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RESULT 3
US-09-945-584-69
; Sequence 69, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 12, 1997
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-584-69

Query Match   100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity   100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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Db      1  MCSRVPLLLPLLLLALGPGVQGCPSGCQCSQOPQTVFCTARQGTTVPRDVPDTVGLYVF   60
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Qy     61  ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE  120

Qy    121  ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLLAGNTRIAQL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLLAGNTRIAQL 180

Qy    181  RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240

Qy    241  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL  300

Qy    301  APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCCPPSTCLNGGTCHLGTRHHLACLCPEG 360
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Db    301  APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCCPPSTCLNGGTCHLGTRHHLACLCPEG 360

Qy    361  FTGLYCESQMGGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQGRYLQGSSVQLRSLR 420
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Db    361  FTGLYCESQMGGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQGRYLQGSSVQLRSLR 420

Qy    421  LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGVPEGBEACGEAHT  480
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Db    421  LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGVPEGBEACGEAHT  480

Qy    481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540
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Db    481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540

Qy    541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECRVPLMGFPGPGLQSPLHAKPYI  598
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Db    541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI  598
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RESULT 4
US-09-944-944-69
; Sequence 69, Application US/09944944
; Patent No. 6929947
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,944
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335

; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
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; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT

Mon Jan 9 06:59:13 2006

us-09-943-780-69.rai

; ORGANISM: Homo Sapien
US-09-944-944-69

Query Match   100.0%;   Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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Db      1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60

Qy     61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE 120

Qy    121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLTRLRLAGNTRIAQL 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLTRLRLAGNTRIAQL 180

Qy    181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
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Db    181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240

Qy    241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300

Qy    301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
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Db    301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360

Qy    361 FTGLYCESQMGQGTRPSPTPVTPRPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
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Db    361 FTGLYCESQMGQGTRPSPTPVTPRPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420

Qy    421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGSEACGEAHT 480
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Db    421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGSEACGEAHT 480

Qy    481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
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Db    481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540

Qy    541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI 598
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI 598
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RESULT 5
US-09-945-587-69
; Sequence 69, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587

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;   CURRENT FILING DATE: 2001-09-26
;   PRIOR APPLICATION NUMBER: 09/866,028
;   PRIOR FILING DATE: 2001-05-25
;   PRIOR APPLICATION NUMBER: 60/067,411
;   PRIOR FILING DATE: December 3, 1997
;   PRIOR APPLICATION NUMBER: 60/069,334
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069935
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,278
;   PRIOR FILING DATE: December 11, 1997
;   PRIOR APPLICATION NUMBER: 60/069,425
;   PRIOR FILING DATE: December 12, 1997
;   PRIOR APPLICATION NUMBER: 60/069,696
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,694
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,702
;   PRIOR FILING DATE: December 16, 1997
;   PRIOR APPLICATION NUMBER: 60/069,870
;   PRIOR FILING DATE: December 17, 1997
;   PRIOR APPLICATION NUMBER: 60/069,873
;   PRIOR FILING DATE: December 17, 1997
;   PRIOR APPLICATION NUMBER: 60/068,017
;   PRIOR FILING DATE: December 18, 1997
;   PRIOR APPLICATION NUMBER: 60/070,440
;   PRIOR FILING DATE: January 5, 1998
;   PRIOR APPLICATION NUMBER: 60/074,086
;   PRIOR FILING DATE: February 9, 1998
;   PRIOR APPLICATION NUMBER: 60/074,092
;   PRIOR FILING DATE: February 9, 1998
;   PRIOR APPLICATION NUMBER: 60/075,945
;   PRIOR FILING DATE: February 25, 1998
;   PRIOR APPLICATION NUMBER: 60/112,850
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 60/113,296
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 60/146,222
;   PRIOR FILING DATE: July 28, 1999
;   PRIOR APPLICATION NUMBER: PCT/US98/19330
;   PRIOR FILING DATE: September 16, 1998
;   PRIOR APPLICATION NUMBER: PCT/US98/25108
;   PRIOR FILING DATE: December 1, 1998
;   PRIOR APPLICATION NUMBER: 09/216,021
;   PRIOR FILING DATE: December 16, 1998
;   PRIOR APPLICATION NUMBER: 09/218,517
;   PRIOR FILING DATE: December 22, 1998
;   PRIOR APPLICATION NUMBER: 09/254,311
;   PRIOR FILING DATE: March 3, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/12252
;   PRIOR FILING DATE: June 22, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/21090
;   PRIOR FILING DATE: September 15, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28409
;   PRIOR FILING DATE: No. 6936254ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28313
;   PRIOR FILING DATE: No. 6936254ember 30, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/28301
;   PRIOR FILING DATE: December1, 1999
;   PRIOR APPLICATION NUMBER: PCT/US99/30095
;   PRIOR FILING DATE: December 16, 1999
;   PRIOR APPLICATION NUMBER: PCT/US00/03565
;   PRIOR FILING DATE: February 11, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/04414
;   PRIOR FILING DATE: February 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/05841
;   PRIOR FILING DATE: March 2, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/08439
;   PRIOR FILING DATE: March 30, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/14042
;   PRIOR FILING DATE: May 22, 2000
;   PRIOR APPLICATION NUMBER: PCT/US00/20710
;   PRIOR FILING DATE: July 28, 2000
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RESULT 6
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens

; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
US-09-945-587-69
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

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Best Local Similarity 100.0%;   Pred. No. 6.6e-217;
Matches 598; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 ENGITMLDASSFAGLPGLQLDLSQNQIASLRLPRLLLLLDLSHNSLLALEPGILDTANVE 120
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Db   61 ENGITMLDASSFAGLPGLQLDLSQNQIASLRLPRLLLLLDLSHNSLLALEPGILDTANVE 120

Qy   121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
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Db   121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180

Qy   181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE 240
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Qy   241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
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Db   241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300

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Db   301 APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360

Qy   361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420
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Db   361 FTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR 420

Qy   421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT 480
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Qy   481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV 540
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Qy   541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI 598
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US-09-063-950-2

Query Match   98.4%;   Score 3083.5; DB 2;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 3.8e-213;
Matches 597; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Db   61 ENGITMLDAGSPAGLPGLQLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy   91 ------------------------------LRLPRLLLLLDLSHNS 105
                                       |||||||||||||||
Db   121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLLDLSHNS 180

Qy   106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
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Db   181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 240

Qy   166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
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Db   241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

Qy   226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
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Db   301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 360

Qy   286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 345
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Db   361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 420

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RESULT 7
US-09-991-181-52
; Sequence 52, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.

```
APPLICANT:  Kljavin,Ivar J.
APPLICANT:  Napier,Mary A.
APPLICANT:  Pan,James
APPLICANT:  Paoni,Nicholas F.
APPLICANT:  Roy, Margaret Ann
APPLICANT:  Stewart, Timothy A.
APPLICANT:  Tumas, Daniel
APPLICANT:  Watanabe, Colin K.
APPLICANT:  Williams, P. Mickey
APPLICANT:  Wood, William I.
APPLICANT:  Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE:  2001-11-16
PRIOR APPLICATION NUMBER: 60/049787          PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1997-06-16                PRIOR APPLICATION NUMBER: 60/088742
PRIOR APPLICATION NUMBER: 60/062250          PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1997-10-17                PRIOR APPLICATION NUMBER: 60/088810
PRIOR APPLICATION NUMBER: 60/065186          PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/065311          PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/066770          PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/075945          PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-03-20                PRIOR APPLICATION NUMBER: 60/088876
PRIOR APPLICATION NUMBER: 60/083322          PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-04-28                PRIOR APPLICATION NUMBER: 60/089105
PRIOR APPLICATION NUMBER: 60/084600          PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-07                PRIOR APPLICATION NUMBER: 60/089440
PRIOR APPLICATION NUMBER: 60/087106          PRIOR FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/087607          PRIOR FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/088217          PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/088655          PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-09                PRIOR APPLICATION NUMBER: 60/090349
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                                             PRIOR FILING DATE: 1998-06-24
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                                             PRIOR APPLICATION NUMBER: 60/090540
                                             PRIOR FILING DATE: 1998-06-24
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Qy   586 PGLQSPLHAKPYI 598
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Db   661 PGLQSPLHAKPYI 673
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Query Match    98.4%;   Score 3083.5;  DB 2;  Length 673;
Best Local Similarity  88.7%;   Pred. No. 3.8e-213;
Matches  597;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy     1 MCSRVPLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF 60
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Qy    91 ----------------------------------LRLPRLLLLDLSHNS 105
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Qy   106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
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Db   181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 240

Qy   166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
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Db   241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

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Db   301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADPGCPATTTTATVPT 360

Qy   286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTC 345
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PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
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PRIOR APPLICATION NUMBER: 60/088021
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/086655
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

Query Match          98.4%;   Score 3083.5;  DB 2;  Length 673;
Best Local Similarity 88.7%;   Pred. No. 3.8e-213;
Matches 597;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

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Db   61  ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF  120

Qy   91  ------------------------------LRLPRLLLLDLSHNS  105
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Db  121  RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS  180

Qy  106  LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  165
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Db  181  LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  240

Qy  166  LTRLRLAGNTRIAQLRPEDLAGLAAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF  225
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Db  241  LTRLRLAGNTRIAQLRPEDLAGLAAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF  300

Qy  226  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT  285
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Db  301  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT  360

Qy  286  TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTC  345
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Db  361  TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTC  420

Qy  346  HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGL  405
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Qy  466  GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR  525
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Qy  526  RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG  585
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Qy  586  PGLQSPLHAKPYI  598
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Db  661  PGLQSPLHAKPYI  673
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; GENERAL INFORMATION:

; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 60/092182
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PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-09
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Qy   91 --------------------------------------LRLPRLLLLDLSHNS 105
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Db  121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLEKLQDNELRALPPLRLPRLLLLDLSHNS 180

Qy  106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 165
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Db  181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG 240

Qy  166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
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Db  241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-06-09
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
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; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17

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;   PRIOR FILING DATE: 1998-07-07
;   PRIOR APPLICATION NUMBER: 60/092182
;   PRIOR FILING DATE: 1998-07-09

Query Match     98.4%;   Score 3083.5;   DB 2;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 3.0e-213;
Matches  597;   Conservative    0;   Mismatches    0;   Indels    1;   Gaps    1;

Qy          1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF  60

Qy         61 ENGITMLDASSFAGLPGLQLLDLSQNQIAS------------------------------  90
              ||||||||| ||||||||||||||| ||||
Db         61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy         91 ------------------------------------LRLPRLLLLDLSHNS 105
                                                  |||||||||||||||
Db        121 RGLRRLERLYLGKNRIRHIQPGAPDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS 180

Qy        106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVVIRGLRG 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVVIRGLRG 240

Qy        166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 225
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPF 300

Qy        226 NCVCPLSWFGPWVRESHVTLASPETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NCVCPLSWFGPWVRESHVTLASPETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT 360

Qy        286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 345
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC 420

Qy        346 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTRPPRSLTLGIEPVSPTSLRVGL 405
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTRPPRSLTLGIEPVSPTSLRVGL 480

Qy        406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP 540

Qy        466 GRVPGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GRVPGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600

Qy        526 RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGECEVPLMGFPG 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSGECEVPLMGFPG 660

Qy        586 PGLQSPLHAKPYI 598
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Db        661 PGLQSPLHAKPYI 673
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;   PRIOR APPLICATION NUMBER: 60/089801
;   PRIOR FILING DATE: 1998-06-18
;   PRIOR APPLICATION NUMBER: 60/089907
;   PRIOR FILING DATE: 1998-06-18
;   PRIOR APPLICATION NUMBER: 60/089908
;   PRIOR FILING DATE: 1998-06-18
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;   PRIOR FILING DATE: 1998-06-19
;   PRIOR APPLICATION NUMBER: 60/089948
;   PRIOR FILING DATE: 1998-06-19
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;   PRIOR FILING DATE: 1998-06-19
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;   PRIOR FILING DATE: 1998-06-22
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;   PRIOR APPLICATION NUMBER: 60/090349
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;   PRIOR FILING DATE: 1998-06-23
;   PRIOR APPLICATION NUMBER: 60/090429
;   PRIOR FILING DATE: 1998-06-24
;   PRIOR APPLICATION NUMBER: 60/090431
;   PRIOR FILING DATE: 1998-06-24
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;   PRIOR FILING DATE: 1998-06-24
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;   PRIOR FILING DATE: 1998-07-01
;   PRIOR APPLICATION NUMBER: 60/091478
;   PRIOR FILING DATE: 1998-07-02
;   PRIOR APPLICATION NUMBER: 60/091544
;   PRIOR FILING DATE: 1998-07-01
;   PRIOR APPLICATION NUMBER: 60/091519
;   PRIOR FILING DATE: 1998-07-02
;   PRIOR APPLICATION NUMBER: 60/091626
;   PRIOR FILING DATE: 1998-07-02
;   PRIOR APPLICATION NUMBER: 60/091633
;   PRIOR FILING DATE: 1998-07-02
;   PRIOR APPLICATION NUMBER: 60/091978
;   PRIOR FILING DATE: 1998-07-07
;   PRIOR APPLICATION NUMBER: 60/091982
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-10

Query Match          10.7%;  Score 337;  DB 2;  Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

Qy    7 LLLPLLLL--------LALGPGVQGCPSGCQCS-QPQTVFCTARQGTTVPRDVPPD  53
          :||:||||    |||:|:|| | :||  : | ||:::|
Db   17 ILLPFVLTAQVWILCAAIAAAASAGPQNCPSVCSSNQFSKVVCTRRGLSEVPQGIPSN  76

Qy   54 TVGLYVFENGITMLDASSFAGLPGLQLDLSQNQIASLR------LPRLLLDLSHNSLL 107
Db   77 TRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLSTELFDNWLT 136

Qy  108 ALEPGILDTAN------------VEALRLAGLG----LQQLDEGLFSRLR 141
Db  137 VIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISEGAFEGLF 196

Qy  142 N----------------LHDLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIA 178
Db  197 NLKYLNLNLGMCNIKDMPNLTPLVGLEELEMSGNHFPEIRPGSFHGLSSLKKLWVM-NSQVS 255

Qy  179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAA--RNPFNCVCPLSWFG 235
Db  256 LIERNAFDGLASLVELNLAHNNLSSLPHD---LFTPLRYLVELHLHHNPWNCDCDILWLA 312

Qy  236 PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
Db  313 WWLRE-YIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSA------PFIMDAPRDLNI 364

Qy  296 LSSSLAP----------TWLSPTAPA-TEAPSPPSTAPPTVGPVPQP----QDCPPSTC 339
Db  365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTC 424

Qy  340 ----------------LNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTP-- 383
Db  425 MGTNVAGNSNASAYLNGSTAELNTSNY--------SFFTTGTGETTEISPEDTTRKY 473

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Db  474 KPVPTTSTGYQPAYTTSTTVLIQ------------TTRVPKQVA 505

Qy  444 EYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLI 503
Db  506 ----------VPATD------TTDKMQTSLDEVMKTTK-----II 529

Qy  504 APALAAVLLAALAAVGAAYCVRR--GRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGP 560
Db  530 IGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAAR----------TVEIIQVD-EDIP 576

Qy  561 KATEGGGEALPSG 573
Db  577 AATSAAATAAPSG 589


RESULT 12
US-09-957-187-10
; Sequence 10, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRochelle, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
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; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
;
SEQ ID NO 10
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-187-10

Query Match          10.7%;  Score 337;  DB 2;  Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

Qy    7 LLLPLLLL--------LALGPGVQGCPSGCQCS-QPQTVFCTARQGTTVPRDVPPD  53
Db   17 ILLPFVLTAQVWILCAAIAAAASAGPQNCPSVCSSNQFSKVVCTRRGLSEVPQGIPSN  76

Qy   54 TVGLYVFENGITMLDASSFAGLPGLQLDLSQNQIASLR------LPRLLLDLSHNSLL 107
Db   77 TRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLSTELFDNWLT 136

Qy  108 ALEPGILDTAN------------VEALRLAGLG----LQQLDEGLFSRLR 141
Db  137 VIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISEGAFEGLF 196

Qy  142 N----------------LHDLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIA 178
Db  197 NLKYLNLNLGMCNIKDMPNLTPLVGLEELEMSGNHFPEIRPGSFHGLSSLKKLWVM-NSQVS 255

Qy  179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAA--RNPFNCVCPLSWFG 235
Db  256 LIERNAFDGLASLVELNLAHNNLSSLPHD---LFTPLRYLVELHLHHNPWNCDCDILWLA 312

Qy  236 PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
Db  313 WWLRE-YIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSA------PFIMDAPRDLNI 364

Qy  296 LSSSLAP----------TWLSPTAPA-TEAPSPPSTAPPTVGPVPQP----QDCPPSTC 339
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Qy  340 ----------------LNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTP-- 383
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Qy  384 RPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLA 443
Db  474 KPVPTTSTGYQPAYTTSTTVLIQ------------TTRVPKQVA 505

Qy  444 EYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLI 503
Db  506 ----------VPATD------TTDKMQTSLDEVMKTTK-----II 529

Qy  504 APALAAVLLAALAAVGAAYCVRR--GRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGP 560
Db  530 IGCFVAVTLLAAAMLIVFYKLRKRHQQRSTVTAAR----------TVEIIQVD-EDIP 576

Qy  561 KATEGGGEALPSG 573
Db  577 AATSAAATAAPSG 589


RESULT 13
US-09-991-053-10
; Sequence 10, Application US/09991053
; Patent No. 6942992
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
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; TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 15966-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 10
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-053-10

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Query Match             10.7%;  Score 337;  DB 2;  Length 653;
Best Local Similarity   23.6%;  Pred. No. 5.1e-16;
Matches 159;  Conservative 77;  Mismatches 231;  Indels 206;  Gaps 25;

Qy    7 LLLPLLLL---------LALGPGVQGCPSGCQCS-QPQTVFCTARQGTTVPRDVPPD 53
          :||| :|                  |:| :
Db   17 ILLPFVYLTAQVWILCAAIAAAAASAGPQNCPSVCSCSNQFSKVVCTRRGLSEVPQGIPSN 76

Qy   54 TVGLYVFENGITMLDASSFAGLPGLQLDLSQNQIASLR------LPRLLLLDLSHNSLL 107
Db   77 TRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLSTLELFDNWLT 136

Qy  108 ALEPGILDTAN----------------VEALRLAGLG----LQQLDEGLFSRLR 141
Db  137 VIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDIGELKKLEYISEGAFEGLF 196

Qy  142 N------------------LHDLDVSDNQLERV-PPVIRGLTRLRLAGNTRIA 178
Db  197 NLKYLNLGMCNIKDMPNLTPLVGLEELEMSGNHFPEIRPGSFHGLSSLKKLWVM-NSQVS 255

Qy  179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAA--RNPFNCVCPLSWFG 235
Db  256 LIERNAFPDGLASLVELNLAHNNLSSLPHD---LFTPLRYLVELHLHHNPWNCDCDILWLA 312

Qy  236 PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
Db  313 WWLRE-YIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSA--------PFIMDAPRDLNI 364

Qy  296 LSSSLAP------------TWLSPTAPA-TEAPSPPSTAPPTVGPVPQP----QDCPPSTC 339
Db  365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTC 424

Qy  340 ------------LNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTP-- 383
Db  425 MGTNVAGNSNASAYLNGSTAELNTSNY-----------SFFTTGTGETTEISPEDTTRKY 473

Qy  384 RPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLA 443
Db  474 KPVPTTSTGYQPAYTTSTTVLIQ------------TTRVPKQVA 505

Qy  444 EYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLI 503

Qy  506 ------------VPATD-----TTDKMQTSLDEVMKTTK-----II 529
Db  504 APALAAVLLALAAVGAAYCVRR--GRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGP 560

Qy  530 IGCFAVTLLAAAMLIVFYKLRKRHQQRSTVTAAR--------TVBIIQVD-EDIP 576
Db  561 KATEGGGEALPSG 573

Db  577 AATSAAATAAPSG 589
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RESULT 14
US-09-520-781-12
; Sequence 12, Application US/09520781
; Patent No. 6689866

; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866e1 Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-12

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Query Match             10.6%;  Score 333;  DB 2;  Length 590;
Best Local Similarity   25.8%;  Pred. 8.7e-16;
Matches 130;  Conservative 60;  Mismatches 187;  Indels 126;  Gaps 18;

Qy    7 LLLPLLLL---------LALGPGVQGCPSGCQCS-QPQTVFCTARQGTTVPRDVPPD 53
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Qy   54 TVGLYVFENGITMLDASSFAGLPGLQLDLSQNQIASLR------LPRLLLLDLSHNSLL 107
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Qy  108 ALEPGILDTAN----------------VEALRLAGLG----LQQLDEGLFSRLR 141
Db  137 VIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDIGELKKLEYISEGAFEGLF 196

Qy  142 N------------------LHDLDVSDNQLERV-PPVIRGLTRLRLAGNTRIA 178
Db  197 NLKYLNLGMCNIKDMPNLTPLVGLEELEMSGNHFPEIRPGSFHGLSSLKKLWVM-NSQVS 255

Qy  179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAA--RNPFNCVCPLSWFG 235
Db  256 LIERNAFPDGLASLVELNLAHNNLSSLPHD---LFTPLRYLVELHLHHNPWNCDCDILWLA 312

Qy  236 PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
Db  313 WWLRE-YIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSA--------PFIMDAPRDLNI 364

Qy  296 LSSSLAP------------TWLSPTAPA-TEAPSPPSTAPPTVGPVPQP----QDCPPSTC 339
Db  365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTC 424

Qy  340 ------------LNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTP- 383
Db  425 MGTNVAGNSNASAYLNGSTAELNTSNY-----------SFFTTGTGETTEISPEDTTRKY 473

Qy  384 RPPRSLTLGIEPVSPTSLRVGLQ 406
Db  474 KPVPTTSTGYQPAYTTSTTVLIQ 496
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RESULT 15
US-09-957-187-12
; Sequence 12, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRochelle, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082

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;   PRIOR FILING DATE: 2000-09-20
;   PRIOR APPLICATION NUMBER: 60/233,798
;   PRIOR FILING DATE: 2000-09-19
;   PRIOR APPLICATION NUMBER: 60/174,485
;   PRIOR FILING DATE: 2000-01-04
;   NUMBER OF SEQ ID NOS: 85
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 12
;   LENGTH: 590
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-957-187-12

Query Match         10.6%;   Score 333;   DB 2;   Length 590;
Best Local Similarity   25.8%;   Pred. No. 8.7e-16;
Matches   130;   Conservative   60;   Mismatches 187;   Indels 126;   Gaps    18;

Qy       7 LLLPLLLL--------------LALGPGVQGCPSGCQCS-QPQTVFCTARQGTTVPRDVPPD  53
           :||||:|:                |  :         |   || ::       |::|:  :
Db      17 ILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCTRRGLSEVPQGIPSN  76

Qy      54 TVGLYVFPNGITMLDASSFAGLPGLQLLDLSQNQIASLR------LPRLLLDLSHNSLL 107
           |       | : ||||    |    :|||         |        |::||||||:||
Db      77 TRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLASLSTLELFDNWLT 136

Qy     108 ALEPGILDTAN--------------------VEALRLAGLG----LQQLDEGLFSRLR 141
           |  :  |  |                      :| ||: |     |  || || |:|:|
Db     137 VIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISEGAFEGLF 196

Qy     142 N---------------------LHDLDVSDNQLERV-PPVIRGLRGLTRLRLLAGNTRIA 178
           |                      ::: :||   |    || |    |||:|||::|:::
Db     197 NLKYLNLGMCNIKDMPNLTPLVGLEELEMSGNHFPEIRPGSFHGLSSLKKLWVM-NSQVS 255

Qy     179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAA---RNPFNCVCPLSWFG 235
           :     |    |   |  ||:::::||::|  |            ||:|| | |  |
Db     256 LIERNAFDGLASLVELNLAHNNLSSLPHD---LFTPLRYLVELHLHHNPWNCDCDILWLA 312

Qy     236 PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
           |:||| :|         |||          |||:|:            :
Db     313 WWLRE-YIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSA-------PFIMDAPRDLNI 364

Qy     296 LSSSLAP----------TWLSPTAPA-TEAPSPPSTAPPTVGPVPQP----QDCPPSTC 339
                             | :           |:
Db     365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTC 424

Qy     340 -----------LNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTP-- 383
                       ||:|         :::
Db     425 MGTNVAGNSNASAYLNGSTAELNTSNY------------SFFTTGEFTEISPEDTTRKY 473

Qy     384 RPPRSLTLGIEPVSPTSLRVGLQ 406
           ::|:  :|        |:
Db     474 KPVPTTSTGYQPAYTTSTTVLIQ 496
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Search completed: January 5, 2006, 13:53:41
Job time : 42 secs

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                      GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:    January 5, 2006, 13:48:58 ; Search time 19 Seconds
                                         (without alignments)
                       3028.296 Million cell updates/sec

Title:          US-09-943-780-69
Perfect score:  3135
Sequence:       1 MCSRVPLLLPLLLLLALGPG.........PLMGFPGPGLQSPLHAKPYI 598

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:    283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :    PIR_80:*
        1:  pir1:*
        2:  pir2:*
        3:  pir3:*
        4:  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	322	10.3	605	2	JC5239	insulin-like growt
2	302	9.6	605	2	A41915	insulin-like growt
3	282	9.0	626	1	NBHUIA	platelet glycoprot
4	281.5	9.0	603	2	JC1282	insulin-like growt
5	278.5	8.9	603	2	JC6128	insulin-like growt
6	278	8.9	1531	2	T42218	slit-1 protein hom
7	264.5	8.4	420	2	A53531	oncofetal trophobl
8	261	8.3	1523	2	T13953	MEGF5 protein - ra
9	255.5	8.1	1469	2	B36665	slit protein 2 pre
10	255.5	8.1	1480	2	A36665	slit protein 1 pre
11	251	8.0	622	2	JC7973	synleurin - human
12	243.5	7.8	312	1	NBHUA2	leucine-rich alpha
13	240	7.7	560	2	A60164	platelet membrane
14	237	7.6	707	2	JC7763	neuronal leucine-r
15	231	7.4	1025	2	T42626	secreted leucine-r
16	222.5	7.1	536	2	A34901	lysine carboxypept
17	214.5	6.8	1535	2	S46224	peroxidasin - frui
18	212.5	6.8	361	2	A53860	chondroadherin pre
19	210.5	6.7	4302	2	A38971	polycystic kidney
20	209	6.7	1091	2	A58532	glial cell membran
21	208.5	6.7	382	2	I39068	proline- arginine-
22	200	6.4	653	2	T25194	hypothetical prote
23	199	6.3	1328	2	T23007	hypothetical prote
24	194.5	6.2	789	2	T28714	hypothetical prote
25	194.5	6.2	1355	2	T28715	hypothetical prote
26	193.5	6.2	421	2	T46266	hypothetical prote
27	193.5	6.2	721	2	E70766	hypothetical prote
28	192.5	6.1	575	2	T29972	hypothetical prote
29	189	6.0	369	2	S20811	proteoglycan I - m
30	189	6.0	369	2	S32793	biglycan precursor
31	189	6.0	839	2	T04859	extensin homolog F
32	188.5	5.9	440	2	A47530	oligodendrocyte-my
33	186	5.9	440	2	A39613	oligodendrocyte-my
34	184	5.8	368	1	BGHUN	biglycan precursor - h
35	183	5.8	662	2	S42799	garp precursor - h
36	182	5.8	369	2	S32559	biglycan precursor
37	181.5	5.7	357	2	S24317	decorin precursor
38	177.5	5.7	2493	2	A55481	adenylate cyclase
39	176.5	5.6	1495	2	T31434	densin-180 - rat
40	175	5.6	343	2	A41748	lumican precursor
41	173	5.5	925	2	JC2003	G protein-coupled
42	172.5	5.5	359	1	NBHUC8	decorin precursor
43	172	5.5	1134	2	T04587	hypothetical prote
44	170.5	5.5	2145	2	JC4747	adenylate cyclase
45	170	5.4	907	2	JE0176	orphan G protein-c
46	169.5	5.4	760	2	T06291	extensin homolog T
47	169	5.4	354	2	A55454	decorin precursor
48	169	5.4	839	2	F75518	hypothetical prote
49	168.5	5.4	907	2	JG0193	G protein-coupled
50	167	5.3	800	2	S37387	internalin A precu
51	167	5.3	1112	2	T10504	disease resistance
52	166.5	5.3	549	2	T41744	hypothetical prote
53	166.5	5.3	800	2	AB1129	internalin A [impo
54	165.5	5.3	360	2	S06280	decorin precursor
55	165.5	5.3	526	2	C84552	hypothetical prote
56	165.5	5.3	1256	2	S60461	gene flightless-I
57	165.5	5.3	1268	2	A49674	flightless-I homol
58	165	5.3	994	2	H96510	probable disease r
59	163.5	5.2	786	2	T01456	extensin homolog F
60	162	5.2	242	2	T14791	hypothetical prote
61	161	5.1	559	2	T42998	Ras-binding protei
62	161	5.1	682	2	A49121	cell-surface molec
63	161	5.1	682	2	A43318	connectin precurso
64	160.5	5.1	2910	2	T42214	otogelin - mouse
65	160	5.1	744	2	E86255	hypothetical prote
66	159.5	5.1	1112	2	T00952	hypothetical prote
67	159	5.1	572	2	T30947	hypothetical prote
68	159	5.1	613	2	A88684	protein AC7.2 [limp
69	159	5.1	702	2	T21148	hypothetical prote
70	159	5.1	1119	2	AD1822	leucine-rich-repea
71	158.5	5.1	738	2	T19938	hypothetical prote
72	158	5.0	1066	2	T15864	hypothetical prote
73	158	5.0	3570	2	T45025	mucin MUC5B, trach
74	156.5	5.0	360	2	I47020	decorin - rabbit
75	156.5	5.0	980	2	H84632	probable receptor-
76	156	5.0	354	2	S29145	decorin precursor
77	156	5.0	594	2	T23841	hypothetical prote
78	155.5	5.0	903	2	T00705	N-chimerin homolog
79	155.5	5.0	1334	2	T50568	probable multi-dom
80	155	4.9	961	2	T23395	hypothetical prote
81	154.5	4.9	1013	2	T10659	probable serine/th
82	154.5	4.9	1143	2	T10636	hypothetical prote
83	154.5	4.9	1192	2	T48499	receptor-like prot
84	154.5	4.9	1495	2	S60255	transcription co-r
85	153.5	4.9	864	2	T08575	protein kinase hom
86	153.5	4.9	894	1	A41527	protein-tyrosine k
87	153	4.9	699	2	C43674	US4 protein - huma
88	152	4.8	786	2	T08664	Toll protein-like
89	151.5	4.8	695	1	JN0898	follitropin recept
90	151	4.8	540	2	T12704	leucine-rich recep
91	151	4.8	1389	2	T13852	gene wheeler prote
92	150.5	4.8	695	1	QRHUFT	receptor-like prot
93	150.5	4.8	1109	2	T18536	receptor-like prot
94	150	4.8	1134	1	A29944	chaoptin precursor
95	149.5	4.8	224	2	T32185	hypothetical prote
96	149.5	4.8	696	2	JC7361	follitropin recept
97	149	4.8	1025	1	A57676	follitropin recept
98	149	4.8	1143	2	B84431	protein kinase Xa2
99	149	4.8	2357	2	A59249	probable receptor
100	148.5	4.7	375	2	S05390	class VII unconven
101	148.5	4.7	610	2	T23836	fibromodulin precu
102	148.5	4.7	680	2	T19939	hypothetical prote

us-09-943-780-69.rpr

No.	Score	Ratio	Len	N	Accession	Description
103	148.5	4.7	890	2	C96654	hypothetical prote
104	148.5	4.7	964	2	T49038	hypothetical prote
105	148.5	4.7	1115	2	S40241	G protein-coupled
106	148	4.7	338	2	S52284	lumicon, secretory
107	148	4.7	1188	2	S49915	extensin-like prot
108	147.5	4.7	316	2	A41781	proteoglycan-Lb -
109	147.5	4.7	1385	2	T13887	tlr protein - frui
110	147	4.7	1964	2	T09059	notch4 - mouse
111	147	4.7	2414	2	A54277	transcription adap
112	146.5	4.7	382	2	T04260	hypothetical prote
113	146.5	4.7	925	2	C84538	probable LRR recep
114	146.5	4.7	1408	2	S16148	gene serrate prote
115	146	4.7	369	2	G83434	translocation prot
116	145.5	4.6	380	2	S71876	fibromodulin - chi
117	145.5	4.6	886	2	S29605	glycoprotein 350/2
118	145.5	4.6	2142	2	B35098	MHC class III hist
119	145	4.6	458	2	T19941	hypothetical prote
120	145	4.6	679	2	T20713	hypothetical prote
121	145	4.6	694	2	JC2237	follitropin recept
122	145	4.6	1839	2	OYBYK	adenylate cyclase
123	144.5	4.6	486	2	B66460	hypothetical prote
124	144.5	4.6	2187	2	T30826	nascent polypeptid
125	144.5	4.6	3149	1	QQBE8	BPLF1 protein - hu
126	144	4.6	695	2	I45896	follicle stimulati
127	144	4.6	1019	2	C96519	probable disease r
128	144	4.6	3020	2	A43932	mucin 2 precursor,
129	143.5	4.6	243	2	B41710	promastigote surfa
130	143.5	4.6	476	2	T27051	hypothetical prote
131	143.5	4.6	496	2	C96832	hypothetical prote
132	143.5	4.6	605	2	T50817	protein serine/thr
133	143.5	4.6	683	2	T24486	hypothetical prote
134	142.5	4.5	1870	2	S37671	MHC class III hist
135	142.5	4.5	1872	2	S36152	MHC class III hist
136	142	4.5	661	2	I56258	RP105 - mouse
137	142	4.5	983	2	G84524	probable disease r
138	141.5	4.5	462	2	D84858	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote
140	141.5	4.5	1029	2	T05050	protein kinase hom
141	141.5	4.5	1051	2	T13174	gp150 protein - fr
142	141	4.5	630	2	AC1129	Internalin B [impo
143	141	4.5	717	2	T33295	hypothetical prote
144	140.5	4.5	376	2	S55275	fibromodulin precu
145	140	4.4	277	2	I60122	rsu-1 homolog - hu
146	140	4.5	474	2	S65763	chitinase (EC 3.2.
147	140	4.5	754	2	A85043	probable LRR recep
148	140	4.5	1029	2	T00712	protein kinase hom
149	139.5	4.4	333	2	T34555	hypothetical prote
150	139.5	4.4	527	2	A75399	hypothetical prote
151	139.5	4.4	539	2	G70520	probable csp prote
152	139.5	4.4	4351	2	T00252	MEGF1 protein - ra
153	139	4.4	581	2	A45551	insect-stage-speci
154	139	4.4	603	2	T24315	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote
156	139	4.4	1088	2	E86312	F11A6.9 protein -
157	139	4.4	2240	2	T37057	probable multi-dom
158	138.5	4.4	342	2	A46743	lumican precursor
159	138.5	4.4	990	2	T14756	hypothetical prote
160	138.5	4.4	1650	2	S53457	dominant autoantig
161	138	4.4	630	2	C39930	hypothetical prote
162	138	4.4	858	2	T00258	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote
164	137.5	4.4	1151	2	I18535	high molecular mas
165	137.5	4.4	4660	2	T42737	gp330 protein prec
166	137	4.4	562	2	T34319	hypothetical prote
167	137	4.4	695	2	JC1493	follitropin recept
168	137	4.4	788	2	AG0786	secreted effector
169	137	4.4	907	1	QQBE21	membrane antigen g
170	137	4.4	4544	1	S02392	alpha-2-macroglobu
171	137	4.4	4545	1	S25111	alpha-2-macroglobu
172	136	4.3	322	2	S72271	proteoglycan Lb pr
173	136	4.3	626	2	AE0123	probable antigenic
174	136	4.3	692	2	A34548	follitropin recept
175	136	4.3	1008	2	D84434	probable receptor-

No.	Len	Ratio	Score	N	Accession	Description
176	4957	4.3	136	2	T03455	ALR protein - huma
177	427	4.3	135.5	2	JC4915	ags protein precur
178	499	4.3	135.5	2	D83333	hypothetical prote
179	1124	4.3	135.5	2	B84742	probable receptor-
180	5262	4.3	135.5	2	T03454	ALR protein - huma
181	601	4.3	135	2	S56144	SH3 domain binding
182	613	4.3	134.5	2	T15489	hypothetical prote
183	847	4.3	134.5	2	F96531	hypothetical prote
184	1039	4.3	134.5	2	T22117	hypothetical prote
185	530	4.3	134	2	A45690	transactivator BBN
186	656	4.3	134	2	B47096	hylB homolog - Str
187	886	4.3	134	2	T40734	probable adenylate
188	277	4.3	133.5	2	S25770	RSP-1 protein - mo
189	384	4.3	133.5	2	A41710	promastigote surfa
190	1068	4.3	133.5	2	H96769	hypothetical prote
191	576	4.2	133	2	T36729	probable serine/th
192	852	4.2	133	2	I51259	tyrosine kinase C
193	932	4.2	133	2	T48489	receptor-like prot
194	1257	4.2	133	2	A88536	protein B0523.5 [i
195	4391	4.2	133	2	A38096	perlecan precursor
196	463	4.2	132.5	2	A36479	milk fat globule m
197	2035	4.2	132.5	2	A40718	host cell factor C
198	3164	4.2	132	1	WMBEH6	UL36 protein - hum
199	346	4.2	131.5	2	T46916	hypothetical prote
200	890	4.2	131.5	2	T00800	disease resistance
201	1097	4.2	131.5	2	A29943	Toll protein precu
202	1286	4.2	131.5	2	A88396	protein M01E10.2 [
203	612	4.2	131	2	T10727	protein kinase Xa2
204	767	4.2	131	2	B84594	probable LRR recep
205	905	4.2	131	2	T00475	probable disease r
206	915	4.2	131	2	T09575	smoothelin - human
207	1095	4.2	131	2	G96746	hypothetical prote
208	1196	4.2	131	2	T09356	brassinosteroid-in
209	448	4.2	130.5	2	T27395	hypothetical prote
210	268	4.1	130	2	T19697	hypothetical prote
211	389	4.1	130	2	H86266	hypothetical prote
212	395	4.1	130	2	H75457	hypothetical prote
213	768	4.1	130	2	T17462	disease resistance
214	800	4.1	130	2	H84740	hypothetical prote
215	315	4.1	129.5	2	T06806	proline rich prote
216	780	4.1	129.5	2	T00366	hypothetical prote
217	861	4.1	129.5	2	A48825	Notch homolog Motc
218	912	4.1	129.5	2	A54423	brevican precursor
219	942	4.1	129.5	2	S23251	protein-tyrosine k
220	1173	4.1	129.5	2	I50620	prockr2 - chicken
221	1469	4.1	129.5	2	T09219	basal transcriptio
222	371	4.1	129	2	S20075	promastigote surfa
223	835	4.1	129	2	T05259	probable disease r
224	910	4.1	129	2	B96770	hypothetical prote
225	1027	4.1	129	2	B85089	receptor protein k
226	1064	4.1	129	2	B86465	probable Protein k
227	1232	4.1	129	2	T05322	hypothetical prote
228	1329	4.1	129	2	A64828	cell division prot
229	1342	4.1	129	2	E85614	cell division prot
230	1342	4.1	129	2	G90750	cell division prot
231	1959	4.1	129	1	AGRT	agrin - rat
232	2321	4.1	129	2	S78549	notch3 protein - h
233	487	4.1	128.5	2	S42442	nuclear protein EB
234	677	4.1	128.5	2	H86208	protein F22G5.26 [
235	727	4.1	128.5	2	C84534	hypothetical prote
236	744	4.1	128.5	2	C84527	probable disease r
237	825	4.1	128.5	2	T29634	hypothetical prote
238	1113	4.1	128.5	2	T00271	hypothetical prote
239	3968	4.1	128.5	2	A44265	trithorax homolog
240	597	4.1	128	2	S72468	probable transcrip
241	967	4.1	128	2	T48210	hypothetical prote
242	1428	4.1	128	2	T08552	lustrin A - Califo
243	1914	4.1	128	2	T42635	tenascin Y precurs
244	750	4.1	127.5	2	D86245	hypothetical prote
245	1120	4.1	127.5	2	B86479	hypothetical prote
246	1784	4.1	127.5	2	C96615	promastigote surfa
247	327	4.1	127	2	S20074	hypothetical prote
248	773	4.1	127	2	T00502	probable receptor-

#					Accession	Description
249	127	4.1	775	1	EDBE11	immediate-early pr
250	127	4.1	800	2	G84740	hypothetical prote
251	127	4.1	1366	2	T35585	probable large Pro
252	127	4.1	1895	2	T06609	disease resistance
253	127	4.1	1955	2	AGCH	agrin precursor -
254	126.5	4.0	268	2	T45516	hypothetical prote
255	126.5	4.0	685	2	JC7570	Delta-4 protein -
256	126.5	4.0	694	2	JC4301	follitropin recept
257	126.5	4.0	862	2	T46289	hypothetical prote
258	126.5	4.0	999	1	S27756	receptor-like prot
259	126.5	4.0	1091	2	S33596	protein-tyrosine k
260	126.5	4.0	1777	2	T34369	hypothetical prote
261	126	4.0	500	2	S49302	AWJL218 protein -
262	126	4.0	865	2	A47282	calcium-binding pr
263	126	4.0	873	2	A47283	calphotin - fruit
264	126	4.0	996	2	F66410	protein F3M18.12 [
265	126	4.0	1152	2	T31911	hypothetical prote
266	126	4.0	1820	2	A55494	latent transformin
267	125.5	4.0	283	2	S13383	hydroxyproline-ric
268	125.5	4.0	548	2	AH1107	internalin H [impo
269	125.5	4.0	635	2	F75477	hypothetical prote
270	125.5	4.0	764	2	A40077	thyrotropin recept
271	125.5	4.0	1003	2	T05898	hypothetical prote
272	125.5	4.0	350	2	S22456	hydroxyproline-ric
273	125.5	4.0	476	2	A36478	surface glycoprote
274	125	4.0	783	2	T45899	receptor protein k
275	125	4.0	818	2	F96586	hypothetical prote
276	125	4.0	991	2	T52400	receptor-like prot
277	125	4.0	1504	2	T49896	glycine/proline-ri
278	125	4.0	2026	1	OYBY	adenylate cyclase
279	124.5	4.0	298	2	B35272	osteoinductive fac
280	124.5	4.0	756	2	T27642	hypothetical prote
281	124.5	4.0	849	2	C97303	hypothetical prote
282	124.5	4.0	910	2	G84648	probable disease r
283	124.5	4.0	977	2	C96745	hypothetical prote
284	124.5	4.0	1011	2	E88451	receptor-kinase li
285	124.5	4.0	2176	2	T13806	protein K10D2.1 [i
286	124	4.0	496	2	D75261	toucan gene protei
287	124	4.0	543	2	S35047	conserved hypothet
288	124	4.0	574	2	T43556	mucin JUL7 - human
289	124	4.0	605	2	AG0123	Wiskott-Aldrich sy
290	124	4.0	729	2	E70803	probable antigenic
291	124	4.0	766	2	B85440	hypothetical prote
292	124	4.0	978	2	E96787	receptor kinase-li
293	124	4.0	1011	2	T45718	protein T4Q12.5 [i
294	124	4.0	1472	2	B54774	receptor-kinase li
295	124	4.0	4135	2	T42629	ATP binding casset
296	123.5	3.9	380	2	T01281	tenascin-X - bovin
297	123.5	3.9	492	2	F86263	hypothetical prote
298	123.5	3.9	656	2	AE1479	probable leucine-r
299	123.5	3.9	690	2	T41296	probable cell surf
300	123	3.9	528	2	T15198	probable alcohol d
301	123	3.9	574	2	T38819	hypothetical prote
302	123	3.9	888	2	S23065	ufo protein - mous
303	123	3.9	1072	2	A37127	microtubule-associ
304	123	3.9	2591	2	T30288	pristinamycin I sy
305	122.5	3.9	303	2	S28264	hydroxyproline-ric
306	122.5	3.9	415	2	T13435	hypothetical prote
307	122.5	3.9	592	2	D70863	extensin homolog F
308	122.5	3.9	699	2	T05225	probable receptor-
309	122.5	3.9	809	2	B84634	hypothetical prote
310	122.5	3.9	845	2	T12537	disease resistance
311	122.5	3.9	1016	2	T30553	collagen alpha 1(V
312	122.5	3.9	2944	2	A54849	osteoglycin precur
313	122	3.9	298	2	JC4130	hypothetical prote
314	122	3.9	326	2	T24722	internalin like pr
315	122	3.9	596	2	AE1515	hypothetical prote
316	122	3.9	623	2	T19876	probable receptor-
317	122	3.9	672	2	B84782	protein F20B24.6 [
318	122	3.9	715	2	G86239	hypothetical prote
319	122	3.9	719	2	T47727	hypothetical prote
320	122	3.9	921	2	B86234	hypothetical prote
321	122	3.9	992	2	T05335	protein-tyrosine k

#					Accession	Description
322	121.5	3.9	432	2	E96712	unknown protein, 6
323	121.5	3.9	519	2	T07026	ethylene receptor
324	121.5	3.9	635	2	T07794	ethylene receptor
325	121.5	3.9	686	2	JC7569	Delta-4 protein -
326	121.5	3.9	760	2	F86387	probable Pto kinas
327	121.5	3.9	902	2	T00588	hypothetical prote
328	121.5	3.9	1251	2	A57293	latent transformin
329	121.5	3.9	1409	2	T37188	presynaptic activi
330	121.5	3.9	2265	1	FNBO	fibronectin - bovi
331	121.5	3.9	2297	2	T34918	polyketide synthas
332	121.5	3.9	2318	2	S45306	notch 3 protein -
333	121.5	3.9	3530	2	A59266	unconventional myo
334	121	3.9	306	2	T52340	cell wall-plasma m
335	121	3.9	480	2	T00971	probable disease r
336	121	3.9	485	2	A33647	sulfated surface g
337	121	3.9	733	2	A45301	microtubule-associ
338	121	3.9	1203	2	A49175	Motch B protein -
339	121	3.9	1520	2	T00273	hypothetical prote
340	121	3.9	2531	2	S18188	notch protein homo
341	120.5	3.8	299	2	A35272	osteoinductive fac
342	120.5	3.8	753	2	JQ0532	OP protein - Kenne
343	120.5	3.8	821	2	AB1126	internalin, peptid
344	120.5	3.8	855	2	T17460	disease resistance
345	120.5	3.8	976	2	B84659	probable receptor-
346	120.5	3.8	976	2	T05897	protein kinase hom
347	120.5	3.8	981	2	T50851	receptor protein k
348	120.5	3.8	987	2	T50850	receptor protein k
349	120.5	3.8	1118	2	A48292	mucin, tracheobron
350	120.5	3.8	1152	2	A33183	microtubule-associ
351	120.5	3.8	1722	2	E89753	protein F1lC7.4 [l
352	120.5	3.8	1778	2	AF1116	internalin protein
353	120.5	3.8	3566	1	A40701	tenascin-X precurs
354	120	3.8	361	2	AH1469	internalin protein
355	120	3.8	376	2	S71558	probable cell wall
356	120	3.8	458	2	T31631	hypothetical prote
357	120	3.8	892	2	T09071	SH3 domains-contai
358	120	3.8	962	2	T04124	receptor-like prot
359	120	3.8	1126	2	T20801	hypothetical prote
360	120	3.8	1224	2	T40765	web1 protein homol
361	119.5	3.8	267	2	S08314	cell wall glycopro
362	119.5	3.8	479	1	A31753	transcription fact
363	119.5	3.8	660	2	T45569	receptor protein k
364	119.5	3.8	1048	1	XPBEA9	large structural p
365	119.5	3.8	1079	2	C96772	probable receptor
366	119.5	3.8	1166	2	F96598	protein F20N2.4 [i
367	119.5	3.8	1400	2	B70963	hypothetical prote
368	119.5	3.8	1596	2	A35927	190K DNA-binding p
369	119.5	3.8	1643	2	T14274	versican precursor
370	119	3.8	164	2	I53641	mucin 5AC - human
371	119	3.8	352	2	S49299	AWJL172 protein -
372	119	3.8	424	2	S27783	hypothetical prote
373	119	3.8	550	2	C75557	hypothetical prote
374	119	3.8	651	2	T42644	hypothetical prote
375	119	3.8	660	1	QOBE3	BHLF1 protein - hu
376	118.5	3.8	808	2	T23129	hypothetical prote
377	118.5	3.8	864	2	D84740	hypothetical prote
378	118.5	3.8	1006	2	T42731	atrophin-1 related
379	118.5	3.8	1045	2	T41119	internalin-relate
380	118.5	3.8	222	2	H96711	hypothetical prote
381	118.5	3.8	400	1	A39822	leukosialin precur
382	118.5	3.8	677	2	E70722	hypothetical prote
383	118.5	3.8	751	2	AC2098	hypothetical prote
384	118.5	3.8	869	2	A71400	probable disease r
385	118.5	3.8	883	2	S57653	brevican precursor
386	118.5	3.8	988	2	T45717	receptor-kinase li
387	118.5	3.8	1173	2	T25893	hypothetical prote
388	118.5	3.8	1356	2	A45445	janusin precursor,
389	118.5	3.8	1607	2	T02837	long chain fatty a
390	118	3.8	294	2	A37232	mucin, tracheal (A
391	118	3.8	599	2	T10798	pherophorin-S - Vo
392	118	3.8	667	2	S74254	homeotic protein s
393	118	3.8	823	2	AD1935	general secretion
394	118	3.8	1134	1	JN0711	protein-tyrosine k

No.	Score	Ratio	Length	Accession	N	Description
395	118	3.8	2471	A49128	2	cell-fate determin
396	117.5	3.7	473	D85041	2	hypothetical prote
397	117.5	3.7	624	A55576	2	collagen alpha 2(X
398	117.5	3.7	660	JW0067	2	chitinase (EC 3.2.
399	117.5	3.7	996	T10725	2	protein kinase Xa2
400	117.5	3.7	1075	D70568	2	hypothetical prote
401	117.5	3.7	1706	I84499	2	zinc finger protei
402	117	3.7	431	T27904	2	hypothetical prote
403	117	3.7	655	A46688	2	hepatocyte growth
404	117	3.7	670	H96707	2	probable receptor
405	117	3.7	678	JC4245	2	transcription fact
406	117	3.7	743	C84633	2	probable disease r
407	117	3.7	801	T29018	2	hypothetical prote
408	117	3.7	1007	C84668	2	probable receptor-
409	117	3.7	1009	D75399	2	probable penicilli
410	117	3.7	1328	T43060	2	agrin - electric r
411	117	3.7	1450	T30273	2	hypothetical prote
412	117	3.7	1574	T13954	2	MEGF6 protein - ra
413	117	3.7	2082	T37056	2	probable multi-dom
414	117	3.7	2232	T34434	2	hypothetical prote
415	116.5	3.7	279	S53363	2	mucin 5AC (clone J
416	116.5	3.7	439	S51939	2	chitinase (EC 3.2.
417	116.5	3.7	621	I38467	2	low density lipopr
418	116.5	3.7	787	T27632	2	hypothetical prote
419	116.5	3.7	794	T27633	2	hypothetical prote
420	116.5	3.7	828	A88860	2	protein ZC518.3 [i
421	116.5	3.7	1048	T31425	2	C-terminal domain-
422	116.5	3.7	1446	A45344	1	immediate-early pr
423	116.5	3.7	2229	T16199	2	hypothetical prote
424	116	3.7	292	S24169	2	mucin - rat
425	116	3.7	652	S71753	2	repellent protein
426	116	3.7	660	AH2348	2	hypothetical prote
427	116	3.7	729	F86308	2	similar to disease
428	116	3.7	771	T02565	2	disease resistance
429	116	3.7	808	B97303	2	hypothetical prote
430	116	3.7	845	T07039	2	Hcr9-0 protein - t
431	116	3.7	907	A24938	2	hypothetical T2 pr
432	116	3.7	1291	T00019	2	period protein hom
433	116	3.7	1494	T14355	2	protein-tyrosine-p
434	116	3.7	1840	T30250	2	GT1 protein - mous
435	116	3.7	2531	A46019	2	notch-1 protein -
436	116	3.7	2555	A40043	2	notch protein homo
437	116	3.7	2774	A43359	2	microtubule-associ
438	115.5	3.7	322	A53715	2	apomucin precursor
439	115.5	3.7	513	AC3061	2	hypothetical prote
440	115.5	3.7	513	D98225	2	hypothetical prote
441	115.5	3.7	528	I47141	2	gastric mucin (clo
442	115.5	3.7	696	T42659	2	extensin-like prot
443	115.5	3.7	805	T49385	2	hypothetical prote
444	115.5	3.7	946	S27921	2	nuclear antigen EB
445	115.5	3.7	1093	I38533	2	AF17 protein - hum
446	115.5	3.7	1268	S52781	2	neurocan - mouse
447	115.5	3.7	1460	EDBEIF	1	immediate-early pr
448	115.5	3.7	2214	T16305	2	hypothetical prote
449	115.5	3.7	3421	WZBEB6	1	367K tegument prot
450	115	3.7	404	T08549	2	hypothetical prote
451	115	3.7	451	S74728	2	hypothetical prote
452	115	3.7	461	T10741	2	hypothetical prote
453	115	3.7	479	S22542	1	transcription fact
454	115.5	3.7	539	AH1216	2	internalin like pr
455	115.5	3.7	766	T01817	2	transcription fact
456	115.5	3.7	838	T08423	2	hypothetical prote
457	115.5	3.7	980	T05414	2	Axin homolog Axil
458	115	3.7	1133	E86308	2	protein kinase hom
459	115	3.7	1220	A56136	2	hypothetical prote
460	115	3.7	2415	A39086	1	jagged protein pre
461	115	3.7	328	JQ0985	2	aggrecan precursor
462	114.5	3.7	409	T11743	2	hydroxyproline-ric
463	114.5	3.7	505	AC1469	2	pP47 protein - pig
464	114.5	3.7	606	T51880	2	internalin like pr
465	114.5	3.7	627	T27123	2	hypothetical prote
466	114.5	3.7	638	T05606	2	protein kinase hom
467	114	3.6	218	T01104	2	disease resistance
468	114	3.6	378	S00842	2	leukosialin precur
469	114	3.6	413	A34888	1	transcription fact
470	114	3.6	555	S20100	1	mullerian inhibiti
471	114	3.6	586	T29695	2	hypothetical prote
472	114	3.6	633	S62057	2	proline-rich prote
473	114	3.6	634	T00388	2	hypothetical prote
474	114	3.6	656	E75468	2	hypothetical prote
475	114	3.6	768	A42755	2	P-selectin precurs
476	114	3.6	1290	T00018	2	period protein hom
477	114	3.6	2225	T26063	2	hypothetical prote
478	113.5	3.6	317	S55316	2	mucin (clone PGM-2
479	113.5	3.6	330	T46256	2	brevican - human (
480	113.5	3.6	538	T01102	2	disease resistance
481	113.5	3.6	896	B43817	2	transforming prote
482	113.5	3.6	907	A86460	2	99.9K hypothetical
483	113.5	3.6	938	QQBE24	1	nuclear antigen EB
484	113.5	3.6	1286	T33476	2	hypothetical prote
485	113.5	3.6	1907	S50893	2	protein-tyrosine-p
486	113.5	3.6	2911	T20566	2	hypothetical prote
487	113	3.6	371	T49908	2	hypothetical prote
488	113	3.6	377	A48018	2	mucin 7 precursor,
489	113	3.6	382	E84527	2	hypothetical prote
490	113	3.6	419	A90088	2	hypothetical prote
491	113	3.6	419	H85729	2	hypothetical prote
492	113	3.6	603	A75373	2	probable N-acetylm
493	113	3.6	979	A35913	2	regulatory factor
494	113	3.6	982	A53253	2	microtubule-associ
495	113	3.6	1002	T46033	2	receptor protein k
496	113	3.6	1025	T45647	2	receptor protein k
497	113	3.6	1069	S27922	2	nuclear antigen EB
498	113	3.6	1247	T42209	2	neural plakophilin
499	113	3.6	1343	AF0611	2	cell division prot
500	113	3.6	2688	I49477	2	alpha-A-crystallin
501	113	3.6	3381	T42389	2	versican precursor
502	112.5	3.6	347	S10571	2	mucin 1 precursor,
503	112.5	3.6	581	G96811	2	unknown protein T1
504	112.5	3.6	731	B86369	2	hypothetical prote
505	112.5	3.6	1075	A57377	2	transcription fact
506	112.5	3.6	1237	AC1583	2	internalin protein
507	112.5	3.6	1680	T01367	2	hypothetical prote
508	112.5	3.6	2479	F87386	2	conserved hypothet
509	112.5	3.6	4006	T09070	2	probable tenascin
510	112	3.6	241	S32359	2	glial growth facto
511	112	3.6	252	T01787	2	thyrotropin recept
512	112	3.6	253	JC1319	2	thyrotropin recept
513	112	3.6	285	A41826	2	probable pheromone
514	112	3.6	383	S53716	2	delta-like homeoti
515	112	3.6	413	S48756	2	transcription fact
516	112	3.6	704	AE2107	2	serine/threonine k
517	112	3.6	731	T04455	2	hypothetical prote
518	112	3.6	742	F84643	2	transcription fact
519	112	3.6	764	QRHURH	1	thyrotropin recept
520	112	3.6	883	S49126	2	brevican precursor
521	112	3.6	960	G84652	2	probable receptor
522	112	3.6	990	T03784	2	probable receptor-
523	112	3.6	1032	T34433	2	hypothetical prote
524	112	3.6	1289	AB2217	2	hypothetical prote
525	112	3.6	224	D72861	2	AcOrf-91 protein -
526	111.5	3.6	383	S32975	2	gene BCRF2 protein
527	111.5	3.5	478	I47154	2	transcription fact
528	111.5	3.5	645	T05251	2	probable disease r
529	111.5	3.5	649	T46500	2	hypothetical prote
530	111.5	3.5	1047	A55617	2	masquerade precurs
531	111.5	3.5	1253	T45787	2	disease resistance
532	111.5	3.5	1298	EDBE75	1	immediate-early pr
533	111.5	3.5	1353	JH0675	2	restrictin precurs
534	111.5	3.5	2649	T51023	2	hypothetical prote
535	111	3.5	274	JC8063	2	heart-restricted 1
536	111	3.5	478	H86459	2	hypothetical prote
537	111	3.5	509	T05260	2	probable disease r
538	111	3.5	518	S50465	2	PAC2 protein - yea
539	111	3.5	548	E70546	2	hypothetical prote
540	111	3.5	603	S28941	2	coagulation factor

Score	Ratio	Index	ID	Count	Num	Ratio	Description
111	3.5	541	S35049	2	610	3.5	mucin JER57 - huma
111	3.5	542	T50150	2	620	3.5	yeast nrd1-like pr
111	3.5	543	QRHUT	1	699	3.5	lutropin-choriogon
111	3.5	544	T17461	2	853	3.5	disease resistance
111	3.5	545	T21138	2	932	3.5	hypothetical prote
111	3.5	546	T48216	1	984	3.5	hypothetical prote
111	3.5	547	I38902	1	1721	3.5	retinoblastoma bin
111	3.5	548	A35844	2	2524	3.5	Xotch protein - Af
110.5	3.5	549	C55066	2	359	3.5	tyrosine decarboxy
110.5	3.5	550	A60058	2	421	3.5	neural cell adhesi
110.5	3.5	551	G86459	2	512	3.5	Hypothetical 55.6
110.5	3.5	552	A58674	2	525	3.5	neurotrophin-3 rec
110.5	3.5	553	T07970	2	533	3.5	aromatic-L-amino-a
110.5	3.5	554	JE0338	2	565	3.5	Frizzled-2 protein
110.5	3.5	555	T01267	1	684	3.5	leucine-rich repea
110.5	3.5	556	S35695	2	803	3.5	neurotrophin-3 rec
110.5	3.5	557	B56708	1	815	3.5	extracellular sign
110.5	3.5	558	T07015	2	855	3.5	Cf-4A protein - to
110.5	3.5	559	S33015	2	872	3.5	hypothetical prote
110.5	3.5	560	A31666	2	992	3.5	hypothetical prote
110.5	3.5	561	T00378	2	1207	3.5	KIAA0641 protein -
110.5	3.5	562	A32901	2	1295	3.5	glp1 protein precu
110.5	3.5	563	T14316	2	1344	3.5	rig-1 protein - mo
110.5	3.5	564	T17412	2	1346	3.5	polyketide synthas
110.5	3.5	565	T00391	2	1736	3.5	hypothetical prote
110.5	3.5	566	T34022	1	2476	3.5	zonadhesin - pig
110	3.5	567	T51437	2	275	3.5	hypothetical prote
110	3.5	568	T04609	2	391	3.5	hypothetical prote
110	3.5	569	S32987	2	549	3.5	hypothetical prote
110	3.5	570	D84889	2	691	3.5	probable receptor-
110	3.5	571	D96711	2	708	3.5	hypothetical prote
110	3.5	572	T02154	2	719	3.5	protein kinase hom
110	3.5	573	I48882	2	764	3.5	thyrotropin recept
110	3.5	574	H70599	2	846	3.5	hypothetical prote
110	3.5	575	T21700	2	846	3.5	hypothetical prote
110	3.5	576	A96770	2	951	3.5	hypothetical prote
110	3.5	577	D96756	2	1123	3.5	receptor-like prot
110	3.5	578	B86143	2	1483	3.5	F6F3.12 protein -
110	3.5	579	A55148	2	1711	3.5	protein-tyrosine-p
110	3.5	580	A24420	1	2703	3.5	notch protein - fr
110	3.5	581	T13049	2	2715	3.5	eyelid - fruit fly
110	3.5	582	T42730	2	3942	3.5	Bassoon protein -
109.5	3.5	583	A86228	2	213	3.5	hypothetical prote
109.5	3.5	584	T10361	2	279	3.5	hypothetical prote
109.5	3.5	585	T29479	2	318	3.5	hypothetical prote
109.5	3.5	586	E71415	2	428	3.5	probable coil wall
109.5	3.5	587	S36553	2	473	3.5	L2 protein - human
109.5	3.5	588	T44768	2	507	3.5	antifreeze glycope
109.5	3.5	589	S57459	2	538	3.5	hook-containing pr
109.5	3.5	590	JC5878	2	558	3.5	plasma hyaluronan-
109.5	3.5	591	S22544	1	583	3.5	transcription fact
109.5	3.5	592	I73633	2	612	3.5	gene trkC protein
109.5	3.5	593	A55178	2	825	3.5	neurotrophin-3 rec
109.5	3.5	594	I73632	2	839	3.5	hypothetical prote
109.5	3.5	595	E97302	2	874	3.5	hypothetical prote
109.5	3.5	596	T21621	2	878	3.5	hypothetical prote
109.5	3.5	597	T19765	2	954	3.5	hypothetical prote
109.5	3.5	598	T47182	2	1299	3.5	genome polyprotein
109.5	3.5	599	RRWPYM	2	1776	3.5	notch homolog - se
109.5	3.5	600	T31070	2	2531	3.5	DNA-binding protei
109.5	3.5	601	A34203	2	2717	3.5	proline-rich prote
109	3.5	602	T05441	1	379	3.5	extensin-like prot
109	3.5	603	D85257	2	379	3.5	CD43 Lp-3 antigen
109	3.5	604	I52842	2	395	3.5	leukosialin CD43 p
109	3.5	605	A43545	2	395	3.5	prpL2 protein.-.hu
109	3.5	606	S52796	2	403	3.5	pistil extensin-li
109	3.5	607	JQ1696	2	426	3.5	hypothetical prote
109	3.5	608	T04868	1	431	3.5	transcription fact
109	3.5	609	A54595	2	437	3.5	receptor-like prot
109	3.5	610	C96756	2	598	3.5	hypothetical prote
109	3.5	611	T42671	1	613	3.5	gene Delta protein
109	3.5	612	S19087	1	833	3.5	hypothetical prote
109	3.5	613	T38236	2	1611	3.5	hypothetical prote

Index	Score	Ratio	Num	Count	ID	Description
614	109	3.5	2809	2	T30213	G-cadherin - sea u
615	108.5	3.5	308	2	JC7125	epidermal growth f
616	108.5	3.5	389	2	S27200	proline-rich prote
617	108.5	3.5	402	2	A84581	probable disease r
618	108.5	3.5	418	2	T15142	hypothetical prote
619	108.5	3.5	499	2	AI1107	internalin E [impo
620	108.5	3.5	514	1	H70699	probable ppp prote
621	108.5	3.5	548	2	I37577	islet cell antigen
622	108.5	3.5	662	2	A45155	mucin FIM-C.1 - Af
623	108.5	3.5	698	2	I39713	celB protein - Agr
624	108.5	3.5	710	1	QQBE22	membrane antigen g
625	108.5	3.5	740	2	B84741	hypothetical prote
626	108.5	3.5	756	2	G86308	Similar to disease
627	108.5	3.5	764	2	A35956	thyrotropin recept
628	108.5	3.5	783	1	A38637	Ras interactor RIN
629	108.5	3.5	825	2	A40026	neurotrophin-3 rec
630	108.5	3.5	855	2	C82983	hypothetical prote
631	108.5	3.5	1011	2	C84524	probable disease r
632	108.5	3.5	1125	2	B41206	microtubule-associ
633	108.5	3.5	1176	2	T49482	hypothetical prote
634	108.5	3.5	1184	1	G01763	atrophin-1 - human
635	108.5	3.5	1344	2	A35175	mucin 1 precursor,
636	108.5	3.5	1357	2	T29265	hypothetical prote
637	108.5	3.5	1487	2	T02850	hypothetical prote
638	108.5	3.5	3707	2	S18252	heparan sulfate pr
639	108	3.4	348	2	JQ0431	hypothetical 35.5K
640	108	3.4	409	2	AG0752	flagellar hook-len
641	108	3.4	511	1	VGBE1K	glycoprotein C - h
642	108	3.4	542	2	I39540	chitinase (EC 3.2.
643	108	3.4	544	2	T17547	proline-rich prote
644	108	3.4	550	2	T36746	probable serine/th
645	108	3.4	638	1	XXAV	dihydrolipoamide S
646	108	3.4	741	2	T05250	probable disease r
647	108	3.4	862	2	S43922	versican - pig-tai
648	108	3.4	996	2	JE0237	apolipoprotein E r
649	108	3.4	1017	2	T31154	probable potassium
650	108	3.4	1217	2	T51140	disease resistance
651	108	3.4	1217	2	T51141	disease resistance
652	108	3.4	2783	1	A41948	alpha-fetoprotein
653	108	3.4	3511	2	A59295	unconventional myo
654	108	3.4	4613	2	T17409	polyketide synthas
655	108	3.4	7576	2	T17428	FKS06 polyketide s
656	107.5	3.4	363	2	H87702	hypothetical prote
657	107.5	3.4	369	2	S20500	hydroxyproline-ric
658	107.5	3.4	414	2	C96770	hypothetical prote
659	107.5	3.4	427	2	S74211	PAS-6/7 protein pr
660	107.5	3.4	536	2	H71563	hypothetical prote
661	107.5	3.4	604	2	S25203	srmR protein - Str
662	107.5	3.4	655	2	G96524	protein TIN15.9 [i
663	107.5	3.4	832	2	A31246	neurogenic protein
664	107.5	3.4	880	2	S00670	neurogenic repetit
665	107.5	3.4	881	2	B98320	cellulose synthase
666	107.5	3.4	1009	2	T45645	receptor kinase-li
667	107.5	3.4	1099	2	A56155	tumor suppressor p
668	107.5	3.4	1206	2	S24407	formin isoform IV
669	107.5	3.4	1324	2	S52863	DNA-binding protei
670	107.5	3.4	1468	2	S11515	formin - mouse
671	107.5	3.4	3534	1	T42567	tegument protein 2
672	107	3.4	176	2	A46606	platelet glycoprot
673	107	3.4	228	2	S53504	extensin-like prot
674	107	3.4	273	2	A28512	fibronectin - chic
675	107	3.4	354	2	A48931	transmembrane glyc
676	107	3.4	358	1	WMBE38	infected cell prot
677	107	3.4	416	1	SKXLAG	dermal gland prote
678	107	3.4	447	2	A39321	mucin - rat (fragm
679	107	3.4	452	2	C41602	transcription fact
680	107	3.4	518	2	F75460	hypothetical prote
681	107	3.4	615	1	KFHU12	coagulation factor
682	107	3.4	650	2	S59630	dystroglycan alpha
683	107	3.4	840	1	S69304	pheromone response
684	107	3.4	915	1	T12526	hypothetical prote
685	107	3.4	1063	2	GNWVR4	structural polypro
686	107	3.4	1376	2	G00043	osteonidogen - hum

#						Description
687	107	3.4	1389	2	I58157	periaxin - rat
688	107	3.4	2723	2	T03221	probable polyketid
689	107	3.4	7463	2	T36248	CDA peptide synthe
690	106.5	3.4	304	2	A32993	transcription fact
691	106.5	3.4	353	2	A41558	N-syndecan - rat (
692	106.5	3.4	505	2	B46629	mucin 6, gastric (
693	106.5	3.4	509	2	D86911	conserved hypothet
694	106.5	3.4	509	2	T10013	probable phosphopr
695	106.5	3.4	517	2	AD1570	internalin, probab
696	106.5	3.4	620	2	S06733	hydroxyproline-ric
697	106.5	3.4	827	2	AC2963	celB protein [limo
698	106.5	3.4	925	2	H96638	protein TIF9.20 [l
699	106.5	3.4	998	2	C75489	conserved hypothet
700	106.5	3.4	1003	2	T13856	ksr protein - frui
701	106.5	3.4	1161	2	S57180	probable membrane
702	106.5	3.4	1184	2	S50832	atrophin-1 - human
703	106.5	3.4	1305	2	AB0168	probable cell divi
704	106.5	3.4	1442	2	T42607	transcription acti
705	106.5	3.4	1892	2	T18314	hypothetical prote
706	106.5	3.4	2090	2	S26058	probable transform
707	106.5	3.4	2453	2	S60254	nuclear receptor c
708	106	3.4	135	2	T49996	AtAGP4 - Arabidops
709	106	3.4	167	2	A33532	mucin SMUC-40 - hu
710	106	3.4	216	2	I51920	mucin - rhesus mac
711	106	3.4	287	2	S65765	chitinase (EC 3.2.
712	106	3.4	405	2	S78691	flagellar hook-len
713	106	3.4	431	2	S47538	acrosin (EC 3.4.21
714	106	3.4	435	2	D41602	transcription fact
715	106	3.4	443	2	B39794	transcription fact
716	106	3.4	449	2	A24993	cellulase (EC 3.2.
717	106	3.4	567	2	A45977	Rab geranylgeranyl
718	106	3.4	666	2	B70803	hypothetical prote
719	106	3.4	701	2	D48613	gag polyprotein -
720	106	3.4	818	2	T01105	disease resistance
721	106	3.4	822	2	T51049	related to nucleol
722	106	3.4	850	2	S56015	gastric mucin MUC5
723	106	3.4	901	2	A49227	sialidase - Actino
724	106	3.4	914	2	T17233	hypothetical prote
725	106	3.4	1064	2	A40136	fibropellin Ia - s
726	106	3.4	1603	2	A48613	gag/pol polyprotei
727	106	3.4	1958	2	B40505	hypothetical prote
728	106	3.4	2554	1	TVFP7L	kinase-related pro
729	106	3.4	3938	2	T42761	Bassoon protein -
730	105.5	3.4	395	2	T01392	leucine-rich repea
731	105.5	3.4	486	2	A41537	DNA-binding protei
732	105.5	3.4	510	2	A42750	insulinoma-associa
733	105.5	3.4	668	2	T05257	probable disease r
734	105.5	3.4	688	2	T04568	protein kinase hom
735	105.5	3.4	695	2	S62400	amphiphysin (clone
736	105.5	3.4	772	2	T13078	KIAA0992 protein -
737	105.5	3.4	780	2	A48143	HF-1 regulatory el
738	105.5	3.4	952	2	S32954	hypothetical prote
739	105.5	3.4	1132	2	A35098	MHC class III hist
740	105.5	3.4	1172	2	T00065	hypothetical prote
741	105.5	3.4	1621	2	T15264	transcription fact
742	105.5	3.4	1712	2	A38261	masking protein pr
743	105.5	3.4	1839	1	RRWPEM	genome polyprotein
744	105.5	3.4	2477	2	S14428	fibronectin precur
745	105.5	3.4	3033	1	JQ1303	genome polyprotein
746	105	3.3	349	2	T05857	hypothetical prote
747	105	3.3	422	2	I37891	interleukin-11 rec
748	105	3.3	454	2	E75291	probable cell wall
749	105	3.3	460	2	T33110	hypothetical prote
750	105	3.3	486	1	A57601	transcription fact
751	105	3.3	511	1	VGBBF4	glycoprotein C - h
752	105	3.3	566	2	T34842	probable transfera
753	105	3.3	620	2	A70525	hypothetical prote
754	105	3.3	658	2	T08153	cysteine proteinas
755	105	3.3	730	2	JC1456	gelatinase B (EC 3
756	105	3.3	764	2	JC5643	thyroid stimulatin
757	105	3.3	847	1	A53800	mixed-lineage prot
758	105	3.3	895	2	I54343	dystroglycan - hum
759	105	3.3	976	2	A36355	protein-tyrosine k

#						Description
760	105	3.3	1133	2	A54164	sterol regulatory
761	105	3.3	1135	2	T30561	Scythe protein - A
762	105	3.3	1136	2	S57845	protein-tyrosine k
763	105	3.3	1456	2	T01397	LTR gag/pol polypr
764	105	3.3	1658	2	D75489	hypothetical prote
765	105	3.3	1844	2	S01956	hypothetical prote
766	105	3.3	2133	2	T30637	hypothetical prote
767	105	3.3	2409	2	A60979	versican precursor
768	105	3.3	2769	2	UIBO	thyroglobulin prec
769	104.5	3.3	329	2	T17033	leucine rich repea
770	104.5	3.3	407	2	C70816	hypothetical prote
771	104.5	3.3	464	2	T35943	probable hydrolyti
772	104.5	3.3	530	2	T32812	hypothetical prote
773	104.5	3.3	639	2	G02919	transcription fact
774	104.5	3.3	662	2	T04856	hypothetical prote
775	104.5	3.3	700	2	A42395	lutropin receptor
776	104.5	3.3	707	2	A34458	gelatinase B (EC 3
777	104.5	3.3	707	2	A53796	gelatinase B (EC 3
778	104.5	3.3	744	2	T35192	probable ABC trans
779	104.5	3.3	755	2	T20950	hypothetical prote
780	104.5	3.3	909	2	QRXLL1	LDL receptor 1 pre
781	104.5	3.3	960	2	S28262	kinesin-related pr
782	104.5	3.3	1117	2	JC4934	delta-crystallin/E
783	104.5	3.3	1194	2	E96624	hypothetical prote
784	104.5	3.3	1241	2	T37190	nephrin - human
785	104.5	3.3	1505	2	JC4851	hypoxia-inducible
786	104.5	3.3	1851	2	T19964	hypothetical prote
787	104.5	3.3	1898	2	S46216	leukocyte antigen-
788	104.5	3.3	2117	2	T36180	CDA peptide synthe
789	104	3.3	232	2	A60095	larval glue protei
790	104	3.3	306	2	I49139	lymphotoxin-beta -
791	104	3.3	318	2	B64900	hypothetical prote
792	104	3.3	326	2	A46676	CD68 homolog macro
793	104	3.3	332	2	S43988	protein phosphatas
794	104	3.3	360	2	S68209	sds22 protein homo
795	104	3.3	365	2	A39481	serum response fac
796	104	3.3	426	2	D88103	protein W10G11.6 [
797	104	3.3	440	2	I49681	glyceraldehyde-3-p
798	104	3.3	470	2	S36536	L2 protein - human
799	104	3.3	537	2	A46611	myosin-binding pro
800	104	3.3	538	2	S65764	chitinase (EC 3.2.
801	104	3.3	593	2	S49525	glycoprotein G - s
802	104	3.3	712	2	I46031	gelatinase B (EC 3
803	104	3.3	895	2	S20582	dystrophin-associa
804	104	3.3	927	2	T24031	hypothetical prote
805	104	3.3	1045	2	T16275	hypothetical prote
806	104	3.3	1547	2	T28657	blackjack protein,
807	104	3.3	1575	2	S68448	synaptojanin, 170K
808	104	3.3	1711	2	T31337	1,4-beta-glucanase
809	104	3.3	1744	2	A54970	tensin, cardiac mu
810	104	3.3	3507	2	T34513	hypothetical prote
811	103.5	3.3	206	2	NBHUB	platelet glycoprot
812	103.5	3.3	264	2	PQ0478	pistil extensin-li
813	103.5	3.3	281	2	D70845	hypothetical prote
814	103.5	3.3	393	2	PQ0470	pistil extensin-li
815	103.5	3.3	411	2	I55604	platelet glycoprot
816	103.5	3.3	419	1	T49292	hypothetical prote
817	103.5	3.3	444	1	A39794	transcription fact
818	103.5	3.3	489	2	F75591	P49 secreted prote
819	103.5	3.3	625	2	A26456	nicotinic acetylch
820	103.5	3.3	654	2	T33044	hypothetical prote
821	103.5	3.3	889	2	F96637	hypothetical prote
822	103.5	3.3	889	2	T20123	hypothetical prote
823	103.5	3.3	968	2	T00353	hypothetical prote
824	103.5	3.3	975	2	I48974	receptor-protein t
825	103.5	3.3	980	2	S54986	regulatory protein
826	103.5	3.3	1020	2	A29355	fibronectin - chic
827	103.5	3.3	1144	2	A54810	TMV resistance pro
828	103.5	3.3	1171	2	T35548	hypothetical prote
829	103.5	3.3	1268	2	T31420	C-terminal domain-
830	103.5	3.3	1590	2	B86398	protein T7N9.24 [i
831	103.5	3.3	1603	2	S23810	collagen alpha 1(X
832	103.5	3.3	1638	2	A42091	transcription acti

No.	Score		Length	Code	Ct	Description
833	103.5	3.3	1733	B45344	1	probable nuclear a
834	103.5	3.3	3739	T17410	2	polyketide synthas
835	103	3.3	168	S52994	2	arabinogalactan-li
836	103	3.3	191	E84740	2	hypothetical prote
837	103	3.3	227	T27905	2	hypothetical prote
838	103	3.3	263	S01360	2	salivary glue prot
839	103	3.3	362	A44083	2	meg protein - Mare
840	103	3.3	367	AC1328	2	internalin protein
841	103	3.3	379	T16213	2	APX-1 protein homo
842	103	3.3	394	C84905	2	probable extensin
843	103	3.3	515	F70904	2	hypothetical prote
844	103	3.3	535	S76953	2	protein kinase [EC
845	103	3.3	550	G70597	2	probable proteinas
846	103	3.3	575	JG0181	2	XllL2 protein - hu
847	103	3.3	611	B86387	2	unknown protein [i
848	103	3.3	648	T35120	2	hypothetical prote
849	103	3.3	701	F48613	2	gag polyprotein -
850	103	3.3	793	JC7390	2	thyroid stimulatin
851	103	3.3	799	TVRTTB	2	nerve growth facto
852	103	3.3	813	T04313	2	protein kinase Xa2
853	103	3.3	851	S67285	2	NUD1 protein - yea
854	103	3.3	863	A55173	2	cf-9 protein precu
855	103	3.3	915	S36327	2	clathrin assembly
856	103	3.3	1040	T29092	2	TSC-22 protein hom
857	103	3.3	1121	A82809	2	exodeoxyribonuclea
858	103	3.3	1199	A40670	2	nuclear envelope p
859	103	3.3	1201	G86441	2	unknown protein [i
860	103	3.3	1275	T33369	2	hypothetical prote
861	103	3.3	1340	A39808	2	proteoglycan core
862	103	3.3	1541	T02831	2	AAA protein L4171.
863	103	3.3	1894	C54689	2	protein-tyrosine-p
864	102.5	3.3	2207	GNNY5P	2	genome polyprotein
865	102.5	3.3	2481	A43908	2	fibronectin - Afri
866	102.5	3.3	3133	S52093	2	hemocytin - silkwo
867	102.5	3.3	217	S01358	2	salivary glue prot
868	102.5	3.3	252	T04739	2	hypothetical prote
869	102.5	3.3	316	T31880	2	hypothetical prote
870	102.5	3.3	338	I53043	2	transforming prote
871	102.5	3.3	352	S17313	2	transcription fact
872	102.5	3.3	371	F70555	2	hypothetical prote
873	102.5	3.3	379	S31719	2	proline-rich prote
874	102.5	3.3	383	B86272	2	protein F16A4.12
875	102.5	3.3	385	S53718	2	homeotic protein d
876	102.5	3.3	421	A54785	2	preadipocyte facto
877	102.5	3.3	507	T30709	2	core protein homol
878	102.5	3.3	627	A32385	2	erythropoietin rec
879	102.5	3.3	674	D75393	2	serine proteinase,
880	102.5	3.3	706	T05264	2	probable serine/th
881	102.5	3.3	730	E30411	1	synapsin Ia - bovi
882	102.5	3.3	760	I52580	1	gelatinase B [EC 3
883	102.5	3.3	904	S07896	2	transcription fact
884	102.5	3.3	907	T46170	2	disease resistance
885	102.5	3.3	942	E96636	2	hypothetical prote
886	102.5	3.3	964	JQ1674	2	protein kinase TMK
887	102.5	3.3	1013	JC5545	2	integrin beta-4 pr
888	102.5	3.3	1115	T46422	1	hypothetical prote
889	102.5	3.3	1223	IJMSNL	1	neural cell adhesi
890	102.5	3.3	1350	T15316	1	hypothetical prote
891	102.5	3.3	1350	G36793	2	glucan 1,4-alpha-g
892	102.5	3.3	1367	S48478	1	hypothetical prote
893	102.5	3.3	1678	T35547	1	xylanase - Caldice
894	102.5	3.3	1779	T31085	1	resistance protein
895	102.5	3.3	1813	T30564	1	protein-tyrosine-p
896	102.5	3.3	1863	S46217	2	integrin beta-4 ch
897	102.5	3.3	1875	A36429	2	genome polyprotein
898	102.5	3.3	2207	S09553	2	hybrid proline-ric
899	102	3.3	301	JQ1663	2	ribosome-binding p
900	102	3.3	307	S36779	1	proline-rich prote
901	102	3.3	317	A28996	2	bcsA 5'-region pro
902	102	3.3	353	B36963	1	hypothetical prote
903	102	3.3	413	T49545	2	hypothetical prote
904	102	3.3	532	S74453	2	DNA-binding protei
905	102	3.3	554	FQHUMP	1	macrophage colony-
906	102	3.3	567	JC5538	2	Rab geranylgeranyl
907	102	3.3	585	B70747	1	probable serine/th
908	102	3.3	650	B87791	2	protein B0207.1 [i
909	102	3.3	670	S22293	2	zinc finger protei
910	102	3.3	715	T12534	2	hypothetical prote
911	102	3.3	722	I48324	2	DELTA-like 1 - mou
912	102	3.3	728	D86278	2	hypothetical prote
913	102	3.3	890	E84846	2	probable receptor-
914	102	3.3	896	A35782	1	cytokine receptor
915	102	3.3	923	A39596	2	progesterone recep
916	102	3.3	963	A55926	2	DNA binding protei
917	102	3.3	1008	T04462	2	hypothetical prote
918	102	3.3	1021	H75423	2	hypothetical prote
919	102	3.3	1032	D83637	2	serine/threonine p
920	102	3.3	1052	B49120	2	protein-tyrosine k
921	102	3.3	1069	D85383	2	hypothetical prote
922	102	3.3	1137	A86335	2	T20H2.9 protein -
923	102	3.3	1166	T13958	2	synGAP-b1 protein
924	102	3.3	1249	T14270	2	Ras-GTPase activat
925	102	3.3	1293	T14259	2	ras GTPase-activat
926	102	3.3	1692	A33988	2	adenylate cyclase
927	102	3.3	1985	S19151	2	hypothetical prote
928	102	3.3	2218	B84683	2	hypothetical prote
929	102	3.3	2437	S42612	2	transmembrane prot
930	102	3.3	2440	S39162	2	transcription coac
931	102	3.3	2441	S39161	2	CREB-binding prote
932	102	3.3	3124	A40020	2	collagen alpha 1(X
933	102	3.3	5147	IJFPTM	1	cadherin-related t
934	101.5	3.2	98	S53367	2	mucin SAC (clone M
935	101.5	3.2	173	T47176	2	hypothetical prote
936	101.5	3.2	244	A40428	2	nonspecific cross-
937	101.5	3.2	372	T29359	2	hypothetical prote
938	101.5	3.2	409	T43599	2	yop targeted effec
939	101.5	3.2	547	B56573	2	nuclear pore compl
940	101.5	3.2	654	C87587	2	hypothetical prote
941	101.5	3.2	657	B84869	2	probable SF16 prot
942	101.5	3.2	710	T44753	2	hypothetical prote
943	101.5	3.2	728	I50719	2	C-Delta-1 - chicke
944	101.5	3.2	833	A87168	2	conserved hypothet
945	101.5	3.2	869	AF2089	2	hypothetical prote
946	101.5	3.2	921	A55384	2	transcription fact
947	101.5	3.2	947	S40495	2	collagen alpha 1(I
948	101.5	3.2	977	G86420	2	probable receptor-
949	101.5	3.2	977	I52657	2	seizure-related pr
950	101.5	3.2	984	A34076	1	protein-tyrosine k
951	101.5	3.2	1034	JC5569	2	serine proteinase
952	101.5	3.2	1039	A85096	2	hypothetical prote
953	101.5	3.2	1429	S06434	2	homeotic protein 1
954	101.5	3.2	1668	T13748	2	sex comb protein -
955	101.5	3.2	1733	S27939	2	tensin - chicken
956	101.5	3.2	4543	A53102	1	alpha-2-macroglobu
957	101	3.2	240	B24264	2	proline-rich prote
958	101	3.2	249	S72619	2	hypothetical prote
959	101	3.2	294	T34537	2	hypothetical prote
960	101	3.2	360	S25561	2	transcription fact
961	101	3.2	373	A44478	2	probable cell grow
962	101	3.2	401	A48423	2	engrailed homeodom
963	101	3.2	482	A44997	2	merozoite surface
964	101	3.2	492	B86911	2	probable penicilli
965	101	3.2	574	B87619	2	sensor histidine k
966	101	3.2	610	A28798	2	myosin-light-chain
967	101	3.2	613	A40497	2	dihydrolipoamide S
968	101	3.2	615	XXHU	2	dihydrolipoamide S
969	101	3.2	628	JQ0110	2	hypothetical 69K p
970	101	3.2	671	D84648	2	probable disease r
971	101	3.2	688	T18263	2	S-layer protein -
972	101	3.2	700	D70951	2	probable UvrD - My
973	101	3.2	739	I56187	2	transcription fact
974	101	3.2	796	T21460	2	hypothetical protein - hu
975	101	3.2	846	QQBEC3	1	HQRF1 protein - hu
976	101	3.2	1043	A56037	2	DNA-binding protei
977	101	3.2	1127	T32404	2	hypothetical prote
978	101	3.2	1257	S28764	2	neurocan precursor

979	101	3.2	1367	2	T33819	hypothetical prote
980	101	3.2	1513	2	A54895	mucin 2, intestina
981	101	3.2	1792	2	A57075	tensin - chicken (
982	101	3.2	2946	2	T15840	hypothetical prote
983	101	3.2	3176	2	CGHU3A	collagen alpha 3 (V
984	100.5	3.2	138	2	D96715	protein F4N2.10 [i
985	100.5	3.2	262	2	T33408	hypothetical prote
986	100.5	3.2	262	2	E88400	protein H34I24.2 [
987	100.5	3.2	269	2	T26957	hypothetical prote
988	100.5	3.2	274	2	T46041	hypothetical prote
989	100.5	3.2	283	2	E88597	protein Y47D3B.6 [
990	100.5	3.2	314	2	T48514	hypothetical prote
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat
992	100.5	3.2	401	2	S65138	glycoprotein antig
993	100.5	3.2	440	2	JC7807	Wiskott-Aldrich sy
994	100.5	3.2	504	2	AG2373	hypothetical prote
995	100.5	3.2	504	2	S56745	mucin (clone pGM31
996	100.5	3.2	512	2	E59437	F02569_2 protein [
997	100.5	3.2	597	2	JQ0107	hypothetical 66K p
998	100.5	3.2	677	2	T39713	zinc finger protei
999	100.5	3.2	798	2	T34248	hypothetical prote
1000	100.5	3.2	906	2	A43817	transforming prote
1001	100.5	3.2	975	2	S33121	homeotic protein C
1002	100.5	3.2	1024	2	T27631	hypothetical prote
1003	100.5	3.2	1030	2	H88859	protein ZC518.2 [i
1004	100.5	3.2	1106	1	TVHUGL	transforming prote
1005	100.5	3.2	1131	2	F96662	hypothetical prote
1006	100.5	3.2	1138	2	S24066	protein-tyrosine k
1007	100.5	3.2	1220	2	T48928	disease resistance
1008	100.5	3.2	1273	2	S58782	SEC31 protein - ye
1009	100.5	3.2	1323	2	T30253	spalt protein - mo
1010	100.5	3.2	2327	2	T42630	aggrecan - bovine
1011	100.5	3.2	2562	2	T14266	xin protein - chic
1012	100.5	3.2	3562	2	A47171	chondroitin sulfat
1013	100.5	3.2	4548	1	S00657	apoprotein(a) (EC
1014	100	3.2	230	2	A56210	neu differentiatio
1015	100	3.2	311	2	B86211	hypothetical prote
1016	100	3.2	334	2	G02409	protein kinase C-b
1017	100	3.2	366	2	S61796	T-cell-specific tr
1018	100	3.2	367	2	A33950	yopM protein - Yer
1019	100	3.2	474	2	S15921	protein TPX-VT3 -
1020	100	3.2	476	2	C39481	serum response fac
1021	100	3.2	510	2	H84824	En/Spm-like transp
1022	100	3.2	535	2	T17212	hypothetical prote
1023	100	3.2	549	2	C87719	protein R119.6 [im
1024	100	3.2	556	2	D70940	probable PPE proce
1025	100	3.2	562	2	S75308	DNA ligase (EC 6.5
1026	100	3.2	596	2	G75457	tetratricopeptide
1027	100	3.2	628	2	S44138	polyadenylate-bind
1028	100	3.2	673	2	AF1143	internalin protein
1029	100	3.2	698	2	T51915	hypothetical prote
1030	100	3.2	698	2	T17261	hypothetical prote
1031	100	3.2	699	2	T09069	probable cAMP-resp
1032	100	3.2	713	2	T44447	neuregulin-3 [impo
1033	100	3.2	725	2	T01268	leucine-rich repea
1034	100	3.2	756	2	C87432	hypothetical prote
1035	100	3.2	776	2	A46583	neuroendocrine-spe
1036	100	3.2	881	2	T01269	serine/threonine-s
1037	100	3.2	1109	2	C84545	probable disease r
1038	100	3.2	1161	2	T45294	hypothetical prote
1039	100	3.2	1182	2	I48378	hairless protein -
1040	100	3.2	1240	2	T06404	resistance complex
1041	100	3.2	1420	2	T37781	probable cytoskele
1042	100	3.2	1687	2	T30176	EGF repeat transme
1043	100	3.2	1791	2	T02345	hypothetical prote
1044	100	3.2	1802	2	T00020	bacterial blight-r
1045	100	3.2	1897	1	TDHULK	leukocyte antigen-
1046	100	3.2	2459	2	AF2136	peptide synthetase
1047	99.5	3.2	108	2	S08315	cell wall protein
1048	99.5	3.2	177	2	T07642	pEARLI 1 protein h
1049	99.5	3.2	230	2	A44074	probable EGF-like
1050	99.5	3.2	280	2	I48713	Phox2 homeodomain
1051	99.5	3.2	293	2	C75421	hypothetical prote

1052	3.2	99.5	352	S05500	2	Ig alpha-1 chain C
1053	3.2	99.5	353	A1HU	1	Ig alpha-1 chain C
1054	3.2	99.5	353	S36438	1	EPPT protein - hyd
1055	3.2	99.5	375	TDHUM4	2	monocyte surface g
1056	3.2	99.5	383	VGBEKG	2	glycoprotein precu
1057	3.2	99.5	387	B49175	2	Notch A protein -
1058	3.2	99.5	392	B48423	2	homeotic protein e
1059	3.2	99.5	393	VGBED2	2	glycoprotein D - h
1060	3.2	99.5	420	T46910	2	hypothetical prote
1061	3.2	99.5	451	JC4199	2	heat-shock protein
1062	3.2	99.5	476	C70986	2	probable serine/th
1063	3.2	99.5	491	F70699	2	probable pbpA prot
1064	3.2	99.5	530	S52215	2	hypothetical prote
1065	3.2	99.5	539	T28770	2	hypothetical prote
1066	3.2	99.5	647	T43952	2	kinesin-like DNA b
1067	3.2	99.5	665	S62328	2	76.4K protein kina
1068	3.2	99.5	702	A86383	2	hypothetical prote
1069	3.2	99.5	802	T24293	2	internalin, probab
1070	3.2	99.5	851	AD1427	2	neural cell adhesi
1071	3.2	99.5	853	IJBONC	1	probable ATP /GTP-
1072	3.2	99.5	886	T35469	2	probable protein k
1073	3.2	99.5	903	T19209	2	hypothetical prote
1074	3.2	99.5	949	T24294	2	glycine cleavage s
1075	3.2	99.5	958	E82994	2	thrombospondin 4 p
1076	3.2	99.5	961	TSHUP4	1	hypothetical prote
1077	3.2	99.5	1013	T33470	2	hypothetical prote
1078	3.2	99.5	1016	T41720	2	hypothetical prote
1079	3.2	99.5	1056	A53767	2	mucin MUC5B, trach
1080	3.2	99.5	1122	T47424	2	hypothetical prote
1081	3.2	99.5	1220	T06403	2	resistance complex
1082	3.2	99.5	1390	T31153	2	polyprotein - Arab
1083	3.2	99.5	1473	T31422	2	C-terminal domain-
1084	3.2	99.5	1742	T17120	2	cellulase (EC 3.2.
1085	3.2	99.5	3869	A48205	2	All-1 protein +GTE
1086	3.2	99	154	PQ0476	1	pistil extensin-li
1087	3.2	99	214	T09854	2	proline-rich cell
1088	3.2	99	307	GSFF3	1	salivary glue prot
1089	3.2	99	329	B41344	2	lutropin-choriogon
1090	3.2	99	329	D41344	2	lutropin-choriogon
1091	3.2	99	331	C41344	2	lutropin-choriogon
1092	3.2	99	358	T01296	2	leucine-rich repea
1093	3.2	99	415	A34170	2	acrosin (EC 3.4.21
1094	3.2	99	428	S45361	2	LRR47 protein - fr
1095	3.2	99	447	T34992	2	probable lipoprote
1096	3.2	99	466	T06416	2	cysteine proteinas
1097	3.2	99	511	AC0941	2	probable ABC trans
1098	3.2	99	543	S25128	2	61K protein - Auto
1099	3.2	99	564	I53106	2	gene gli protein -
1100	3.2	99	569	F75381	2	probable two-compo
1101	3.2	99	616	C75588	2	conserved hypothet
1102	3.2	99	638	T51383	2	receptor protein k
1103	3.2	99	641	C84726	2	probable receptor-
1104	3.2	99	686	F96542	2	probable protein k
1105	3.2	99	696	A41344	2	lutropin-choriogon
1106	3.2	99	701	S61239	2	hypothetical prote
1107	3.2	99	770	S30293	2	transcription fact
1108	3.2	99	814	JC7389	2	thyroid stimulatin
1109	3.2	99	860	C86203	2	hypothetical prote
1110	3.2	99	940	H86420	2	probable receptor-
1111	3.2	99	963	T19140	2	hypothetical prote
1112	3.2	99	1000	C82630	2	serine proteinase
1113	3.2	99	1097	T49187	2	hypothetical prote
1114	3.2	99	1147	T42627	2	ADP-ribosylation f
1115	3.2	99	1217	T52348	2	disease resistance
1116	3.2	99	1317	T03748	2	apoptosis associat
1117	3.2	99	1405	T04426	2	hypothetical prote
1118	3.2	99	1532	A61262	2	collagen alpha 1(X
1119	3.2	99	1538	E70874	2	probable ppsB prot
1120	3.2	99	1694	S50065	2	sialoadhesin - mou
1121	3.2	99	1799	S44920	2	ZK688.5 protein -
1122	3.2	99	2029	TDFFLK	1	protein-tyrosine-p
1123	3.2	99	2088	E71436	2	hypothetical prote
1124	3.2	99	6420	T30283	2	polyketide synthas

No.	%	Ver	Len	N	ID	Description
1125	98.5	3.1	230	2	T22763	hypothetical prote
1126	98.5	3.1	254	2	D88560	protein F58A4.1 [li
1127	98.5	3.1	342	2	I77461	luteinizing hormon
1128	98.5	3.1	349	2	T15422	hypothetical prote
1129	98.5	3.1	379	2	S50125	larval glue protei
1130	98.5	3.1	385	2	T18180	proline-rich prote
1131	98.5	3.1	393	2	S62335	I71-7 protein - fr
1132	98.5	3.1	434	2	A35005	u-plasminogen acti
1133	98.5	3.1	464	2	D72653	hypothetical prote
1134	98.5	3.1	486	2	B39481	serum response fac
1135	98.5	3.1	514	2	A44100	cell adhesion mole
1136	98.5	3.1	633	2	T47346	receptor protein k
1137	98.5	3.1	700	2	I77463	luteinizing hormon
1138	98.5	3.1	700	2	A49744	lutropin-choriogon
1139	98.5	3.1	707	2	A46302	PTB-associated spl
1140	98.5	3.1	770	2	T22808	hypothetical prote
1141	98.5	3.1	803	2	F59433	RhoGAP protein [im
1142	98.5	3.1	837	2	A42112	mucin-like peptide
1143	98.5	3.1	862	2	E88594	protein Y48A6B.11
1144	98.5	3.1	885	2	B86257	NBS/LRR disease re
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -
1146	98.5	3.1	947	2	T26314	hypothetical prote
1147	98	3.1	1087	2	T31100	probable potassium
1148	98	3.1	1272	2	T30248	fragile X mental r
1149	98	3.1	1281	2	T00346	hypothetical prote
1150	98	3.1	1309	2	T00078	probable RNA-direc
1151	98	3.1	1396	2	A44453	translation initia
1152	98	3.1	1774	2	B56101	collagen alpha 1(X
1153	98	3.1	2180	2	T29764	hypothetical prote
1154	98	3.1	2339	2	A42566	omega-conotoxin-se
1155	98	3.1	182	2	T07641	pEARLI 1 protein h
1156	98	3.1	291	2	AF0123	probable antigenic
1157	98	3.1	296	2	A56943	sensory/motor neur
1158	98	3.1	303	2	S40973	hypothetical prote
1159	98	3.1	352	2	S09266	Ig alpha chain C r
1160	98	3.1	416	2	A42879	advanced glycosyla
1161	98	3.1	442	2	S50062	cell wall glycopro
1162	98	3.1	499	2	AI2449	hypothetical prote
1163	98	3.1	514	2	A56201	transcription fact
1164	98	3.1	534	2	S21961	proline-rich prote
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.
1166	98	3.1	538	2	I68093	PRR2 delta - human
1167	98	3.1	538	2	A70836	hypothetical prote
1168	98	3.1	553	2	A42499	mullerian inhibiti
1169	98	3.1	560	1	WFHUM	mullerian inhibiti
1170	98	3.1	605	2	S48940	hypothetical prote
1171	98	3.1	614	2	S27962	modulator recognit
1172	98	3.1	631	2	C89243	protein F28C1.3 [i
1173	98	3.1	631	2	T21471	hypothetical prote
1174	98	3.1	715	2	S76492	lipoprotein nlpD -
1175	98	3.1	728	2	H59435	phosphoinositide-3
1176	98	3.1	750	2	T42614	probable envelope
1177	98	3.1	788	1	QQBEE3	HHLF1 protein - hu
1178	98	3.1	856	2	T43631	serine/threonine k
1179	98	3.1	889	2	C86257	resistance to Pseu
1180	98	3.1	896	2	S36326	clathrin assembly
1181	98	3.1	1006	2	JC5526	kinase-defective E
1182	98	3.1	1216	2	T34101	hypothetical prote
1183	98	3.1	1372	2	T25933	hypothetical prote
1184	98	3.1	1522	2	H88380	protein T22F7.3 [i
1185	98	3.1	1873	2	A55645	calcium channel, v
1186	98	3.1	2115	2	S38480	nonstructural prot
1187	98	3.1	3190	2	T13828	CREB-binding prote
1188	98	3.1	3623	2	T08618	intrinsic factor-B
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch
1190	98	3.1	3871	2	T22812	hypothetical prote
1191	98	3.1	5069	2	T17464	rifamycin polyketi
1192	97.5	3.1	215	2	S55925	probable arabinoga
1193	97.5	3.1	266	1	A35037	insulin-like growt
1194	97.5	3.1	268	2	S71830	transcription coac
1195	97.5	3.1	277	2	A46241	interferon respons
1196	97.5	3.1	306	2	T09067	extensin-like prot
1197	97.5	3.1	338	1	TVMSFB	transforming prote
1198	97.5	3.1	362	2	S22395	fetuin precursor -
1199	97.5	3.1	429	2	JC4965	elk1 protein - mou
1200	97.5	3.1	460	2	T23087	hypothetical hormon
1201	97.5	3.1	464	2	S22697	extensin - Volvox
1202	97.5	3.1	497	2	F83634	hypothetical prote
1203	97.5	3.1	511	2	T43282	alp21 protein - fi
1204	97.5	3.1	521	2	S54266	glycoprotein gC -
1205	97.5	3.1	531	2	B55066	tyrosine decarboxy
1206	97.5	3.1	563	2	A75594	ferredoxin-nitrite
1207	97.5	3.1	574	1	A48501	probable protein-l
1208	97.5	3.1	587	2	T41653	probable transcrip
1209	97.5	3.1	614	2	T33149	hypothetical prote
1210	97.5	3.1	626	2	B70754	probable serine/th
1211	97.5	3.1	627	1	JC6534	protein kinase 1 (
1212	97.5	3.1	627	2	AB0535	hypothetical prote
1213	97.5	3.1	631	1	A36749	transcription fact
1214	97.5	3.1	662	2	D40228	neurexin II-beta p
1215	97.5	3.1	676	1	EDBE23	immediate-early pr
1216	97.5	3.1	710	2	D96728	hypothetical prote
1217	97.5	3.1	754	2	AC2807	OmpA family protei
1218	97.5	3.1	754	2	B97586	hypothetical prote
1219	97.5	3.1	814	2	G02390	disintegrin-like m
1220	97.5	3.1	817	2	S51342	verprolin - yeast
1221	97.5	3.1	830	2	T17672	chitinase-like pro
1222	97.5	3.1	893	2	H96651	protein T3P18.19 [
1223	97.5	3.1	909	1	A54809	disease resistance
1224	97.5	3.1	921	2	AE0332	conserved hypothet
1225	97.5	3.1	929	2	T52517	hypothetical prote
1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1227	97.5	3.1	1006	2	G86292	hypothetical prote
1228	97.5	3.1	1258	2	JC5765	inositol polyphosp
1229	97.5	3.1	1392	2	T51947	probable transcrip
1230	97.5	3.1	1715	2	C40228	neurexin II-alpha
1231	97.5	3.1	1748	1	JQ1555	genome polyprotein
1232	97	3.1	191	2	F84522	probable proline-r
1233	97	3.1	238	2	T23867	hypothetical prote
1234	97	3.1	238	2	T26419	hypothetical prote
1235	97	3.1	330	2	T05717	probable extensin
1236	97	3.1	355	2	B26883	neural cell adhesi
1237	97	3.1	357	2	A39364	GDF-1 embryonic gr
1238	97	3.1	379	2	AE3003	conserved hypothet
1239	97	3.1	395	2	A86166	protein F21B7.6 [i
1240	97	3.1	397	2	T00914	leucine-rich repea
1241	97	3.1	400	2	A28172	spasmolysin precur
1242	97	3.1	421	1	S11674	acrosin (EC 3.4.21
1243	97	3.1	428	1	TVHUEK	transforming prote
1244	97	3.1	452	2	D98280	hypothetical 28.0K
1245	97	3.1	459	2	T35317	probable serine/th
1246	97	3.1	483	2	T02226	NBS-LRR type resis
1247	97	3.1	530	2	D97302	hypothetical prote
1248	97	3.1	530	2	G70904	hypothetical prote
1249	97	3.1	601	2	D89711	protein F40E10.4 [
1250	97	3.1	601	2	T22025	hypothetical prote
1251	97	3.1	632	2	T02627	hypothetical prote
1252	97	3.1	701	1	POFV1R	gag polyprotein -
1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1254	97	3.1	966	2	D96662	hypothetical prote
1255	97	3.1	967	2	G96637	hypothetical prote
1256	97	3.1	1123	2	A39962	kinase-related tra
1257	97	3.1	1214	2	T47438	disease resistance
1258	97	3.1	1265	1	A37967	neural cell adhesi
1259	96.5	3.1	1690	2	T35694	ATP dependent DNA
1260	96.5	3.1	1734	2	A54602	microtubule-associ
1261	96.5	3.1	2055	2	T00093	hypothetical prote
1262	96.5	3.1	2205	1	GNNY2W	genome polyprotein
1263	96.5	3.1	3034	2	T14119	seven-pass transme
1264	96.5	3.1	346	2	S19129	proline-rich prote
1265	96.5	3.1	350	2	B75341	peptidyl-prolyl ci
1266	96.5	3.1	419	2	G70602	hypothetical prote
1267	96.5	3.1	430	2	I48755	insulin-like growt
1268	96.5	3.1	444	2	B36389	transcription fact
1269	96.5	3.1	485	1	S22543	transcription fact
1270	96.5	3.1	487	2	F70765	hypothetical prote

No.	%	Score	Len	Accession	N	Description
1271	96.5	3.1	514	A31643	2	cell adhesion 80K
1272	96.5	3.1	528	B75310	2	conserved hypothet
1273	96.5	3.1	574	B35149	2	ipaH protein - Shi
1274	96.5	3.1	598	T42070	2	protein serine/thr
1275	96.5	3.1	635	F70874	2	probable membrane
1276	96.5	3.1	637	A75342	2	hypothetical prote
1277	96.5	3.1	646	T34532	2	hypothetical prote
1278	96.5	3.1	654	T45017	2	chemotaxis histidi
1279	96.5	3.1	669	T08827	2	hypothetical prote
1280	96.5	3.1	796	E96654	2	hypothetical prote
1281	96.5	3.1	825	EDBEXD	1	immediate-early pr
1282	96.5	3.1	1021	A86421	2	Receptor-like seri
1283	96.5	3.1	1209	T00373	2	hypothetical prote
1284	96.5	3.1	1241	T18311	2	hypothetical prote
1285	96.5	3.1	1557	T02859	2	probable serine/th
1286	96.5	3.1	2282	T42717	2	DNA-binding protei
1287	96.5	3.1	2352	T30201	2	Notch homolog prot
1288	96.5	3.1	26926	I38344	1	titin, cardiac mus
1289	96	3.1	214	T10737	2	extensin-like cell
1290	96	3.1	240	A24264	2	proline-rich prote
1291	96	3.1	287	C75494	2	cell division prot
1292	96	3.1	346	JA0159	2	cysteine proteinas
1293	96	3.1	445	T05887	2	hypothetical prote
1294	96	3.1	451	D88395	2	protein F53A3.6 [i
1295	96	3.1	483	S12741	2	transcription fact
1296	96	3.1	537	FOMVGV	1	gag polyprotein -
1297	96	3.1	580	T43481	2	probable mucin DKF
1298	96	3.1	594	S33561	2	ref(2)P protein -
1299	96	3.1	598	T48822	2	hypothetical prote
1300	96	3.1	635	WMBEW6	1	capsid protein - h
1301	96	3.1	858	IURTNC	1	neural cell adhesi
1302	96	3.1	883	A96662	2	hypothetical prote
1303	96	3.1	907	AD2951	2	cell division prot
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1305	96	3.1	969	A75634	2	McrB-related prote
1306	96	3.1	1216	T26104	2	hypothetical prote
1307	96	3.1	1231	S30185	2	insulin receptor s
1308	96	3.1	1544	E59431	2	phosphoinositide-b
1309	96	3.1	1615	B49502	2	MEGF8 protein - hu
1310	96	3.1	1737	T00209	2	protein-tyrosine-p
1311	96	3.1	1767	A49502	2	protein-tyrosine-p
1312	96	3.1	1844	RKWPTM	1	genome polyprotein
1313	96	3.1	2529	A56923	2	transcription fact
1314	96	3.1	5376	T42215	2	zonadhesin - mouse
1315	95.5	3.0	188	D29149	2	proline-rich prote
1316	95.5	3.0	284	F95320	2	conserved hypothet
1317	95.5	3.0	366	TDPMSM4	1	monocyte surface g
1318	95.5	3.0	382	S75823	2	threonine synthase
1319	95.5	3.0	384	S51796	2	vasodilator-stimul
1320	95.5	3.0	435	T46443	2	hypothetical prote
1321	95.5	3.0	451	S71754	2	cellular hepatitis
1322	95.5	3.0	479	D70676	2	probable PE protei
1323	95.5	3.0	486	AB2975	2	succinate semialde
1324	95.5	3.0	486	A98308	2	attK protein (U594
1325	95.5	3.0	501	S76563	2	hypothetical prote
1326	95.5	3.0	507	A46713	2	erythropoietin rec
1327	95.5	3.0	553	C75318	2	hypothetical prote
1328	95.5	3.0	570	A48836	2	fibropellin C prec
1329	95.5	3.0	571	T43456	2	hypothetical prote
1330	95.5	3.0	573	B70726	2	probable secD - My
1331	95.5	3.0	624	T49366	2	myocyte-specific e
1332	95.5	3.0	630	T31798	2	hypothetical prote
1333	95.5	3.0	650	S44806	2	F10E9.6 protein -
1334	95.5	3.0	685	C55591	2	serine/threonine-s
1335	95.5	3.0	710	S70965	1	E75 B steroid rece
1336	95.5	3.0	722	T22359	2	hypothetical prote
1337	95.5	3.0	749	E87594	2	hypothetical prote
1338	95.5	3.0	790	TVHUTT	1	nerve growth facto
1339	95.5	3.0	880	D89756	2	protein T23B7.2b [
1340	95.5	3.0	943	E84429	2	probable receptor-
1341	95.5	3.0	987	A54092	2	protein-tyrosine k
1342	95.5	3.0	1027	I38759	2	zinc finger/leucin
1343	95.5	3.0	1054	A30239	2	hydroxymethylgluta
1344	95.5	3.0	1159	I38465	2	probable potassium
1345	95.5	3.0	1255	T11065	2	diaphanous protein
1346	95.5	3.0	1256	T03096	2	CDO protein - rat
1347	95.5	3.0	1331	T49813	2	related to gastric
1348	95.5	3.0	1630	T00390	2	KIAA0614 protein -
1349	95.5	3.0	2761	T21064	2	hypothetical prote
1350	95	3.0	175	I38808	2	neu differentiatio
1351	95	3.0	227	C29149	2	proline-rich prote
1352	95	3.0	227	G70555	2	hypothetical prote
1353	95	3.0	239	S25618	2	hypothetical prote
1354	95	3.0	241	D43273	2	heregulin precurso
1355	95	3.0	273	C70551	2	hypothetical prote
1356	95	3.0	326	A59232	2	ABA-responsive pro
1357	95	3.0	338	T06336	2	proline-rich prote
1358	95	3.0	385	I39498	1	GTP cyclohydrolase
1359	95	3.0	413	T52617	2	hypothetical protei
1360	95	3.0	477	S53362	2	mucin 5AC (clone J
1361	95	3.0	494	A29079	2	lymphocyte surface
1362	95	3.0	502	A55197	2	Wiskott-Aldrich sy
1363	95	3.0	636	I61718	2	neu differentiatio
1364	95	3.0	653	E84682	2	hypothetical prote
1365	95	3.0	662	I61722	2	neu differentiatio
1366	95	3.0	667	T17221	2	hypothetical prote
1367	95	3.0	673	T48012	2	hypothetical prote
1368	95	3.0	705	A35621	2	spore germination
1369	95	3.0	712	G02512	2	interleukin-1 rece
1370	95	3.0	760	T16726	2	hypothetical prote
1371	95	3.0	776	C96554	2	unknown protein [i
1372	95	3.0	799	T48889	2	serine/threonine p
1373	95	3.0	846	S52418	2	GTP-binding regula
1374	95	3.0	891	G84693	2	probable proline-r
1375	95	3.0	901	A44825	2	phosphoprotein, sy
1376	95	3.0	903	S60257	2	meltrin alpha - mo
1377	95	3.0	943	T34847	2	probable transcrip
1378	95	3.0	1024	S18251	2	collagen alpha 1(X
1379	95	3.0	1209	T13153	2	hypothetical prote
1380	95	3.0	1324	T14070	2	transcription fact
1381	95	3.0	1474	B85188	2	peptide synthetase
1382	95	3.0	1616	G70668	2	retrotransposon li
1383	95	3.0	1731	AB3045	2	polyketide synthas
1384	95	3.0	1731	B98241	2	ice nucleation pro
1385	95	3.0	1770	T18551	2	hypothetical prote
1386	95	3.0	1806	CGHU1E	1	saframycin Mx1 syn
1387	95	3.0	2090	T30075	2	collagen alpha 1(X
1388	95	3.0	2148	A56011	2	hypothetical prote
1389	95	3.0	2274	T30258	2	probable transcrip
1390	95	3.0	3084	MMMSA	1	adenomatous polypo
1391	94.5	3.0	211	T03381	2	laminin alpha-1 ch
1392	94.5	3.0	255	B75309	2	high sulfur zein p
1393	94.5	3.0	270	S31096	2	hypothetical prote
1394	94.5	3.0	277	E87649	2	proline-rich prote
1395	94.5	3.0	298	I38857	2	hypothetical prote
1396	94.5	3.0	301	H87533	2	microtubule-associ
1397	94.5	3.0	358	D87684	2	peptidase, M23/M37
1398	94.5	3.0	376	A61188	2	transcription regu
1399	94.5	3.0	393	H82988	2	probable transcrip
1400	94.5	3.0	464	E82283	2	conserved hypothet
1401	94.5	3.0	569	A83557	2	hypothetical prote
1402	94.5	3.0	630	T19128	2	probable amidase P
1403	94.5	3.0	665	A39344	2	hypothetical prote
1404	94.5	3.0	708	E75461	2	tumor-associated m
1405	94.5	3.0	719	JC4364	2	probable cell wall
1406	94.5	3.0	860	T33170	2	gelatinase B (EC 3
1407	94.5	3.0	921	I48839	2	tenascin-X - mouse
1408	94.5	3.0	985	S42617	2	collagen alpha 1(I
1409	94.5	3.0	1006	T06049	2	hypothetical prote
1410	94.5	3.0	1092	T00050	2	hypothetical prote
1411	94.5	3.0	1191	JN0635	1	neural cell adhesi
1412	94.5	3.0	1487	T13850	2	gene u-shaped prot
1413	94.5	3.0	1690	EDBBE1	1	immediate-early pr
1414	94.5	3.0	2062	CGHU1B	1	collagen alpha 4(I
1415	94.5	3.0	2302	G96602	2	probable receptor-
1416	94.5	3.0		T14328	2	protein-tyrosine-p

1417	94.5	3.0	2386	1	FNHU	fibronectin precur
1418	94.5	3.0	2484	2	T26216	hypothetical prote
1419	94.5	3.0	2607	2	T26215	hypothetical prote
1420	94	3.0	157	2	T02034	early light-induce
1421	94	3.0	263	2	S57346	interleukin 15 rec
1422	94	3.0	277	2	E72564	hypothetical prote
1423	94	3.0	293	2	T22919	hypothetical prote
1424	94	3.0	329	2	T10064	cyokinin-induced
1425	94	3.0	338	2	S28004	probable cell surf
1426	94	3.0	346	2	S76923	hypothetical prote
1427	94	3.0	356	2	A96826	T8K14.10 [imported
1428	94	3.0	421	2	T38309	probable cell wall
1429	94	3.0	456	2	A40492	early growth respo
1430	94	3.0	466	2	A36389	transcription fact
1431	94	3.0	476	2	B44997	merozoite surface
1432	94	3.0	522	2	S41819	nucleoporin p62 -
1433	94	3.0	550	2	C75286	hypothetical prote
1434	94	3.0	590	2	B36789	hypothetical prote
1435	94	3.0	639	2	I61719	neu differentiatio
1436	94	3.0	648	2	S50856	whn protein - rat
1437	94	3.0	677	2	JC7303	pectate lyase (EC
1438	94	3.0	693	1	A41090	serine/threonine-s
1439	94	3.0	791	2	S67265	hypothetical prote
1440	94	3.0	811	2	T36581	probable transmemb
1441	94	3.0	862	2	S51493	major nitrogen reg
1442	94	3.0	865	1	D70986	probable ABC trans
1443	94	3.0	878	1	A40091	interleukin-3 rece
1444	94	3.0	898	2	A40114	fasciclin II precu
1445	94	3.0	918	2	JC4361	scavenger receptor
1446	94	3.0	927	2	A48085	transcription fact
1447	94	3.0	939	2	C70876	hypothetical prote
1448	94	3.0	979	2	A70848	probable membrane
1449	94	3.0	1007	2	G96606	disease resistance
1450	94	3.0	1137	2	G70868	probable regulator
1451	94	3.0	1236	2	E70977	hypothetical prote
1452	94	3.0	1320	2	JC5530	TCOF1 protein - mo
1453	94	3.0	1331	2	A48954	mannan endo-1,4-be
1454	94	3.0	1335	2	T18289	racGAP protein - s
1455	94	3.0	1429	2	T13720	gene expanded prot
1456	94	3.0	1549	2	T11974	glutamate synthase
1457	94	3.0	1560	2	T00080	hypothetical prote
1458	94	3.0	2153	2	T30074	hypothetical prote
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1460	93.5	3.0	278	2	T27610	hypothetical prote
1461	93.5	3.0	299	2	G70784	probable mmpS3 pro
1462	93.5	3.0	305	2	T46721	hypothetical prote
1463	93.5	3.0	352	2	T06482	probable cell wall
1464	93.5	3.0	362	2	S61924	cyst wall protein
1465	93.5	3.0	391	2	I50702	transcription fact
1466	93.5	3.0	458	2	B87335	hypothetical prote
1467	93.5	3.0	461	1	A35356	tumor necrosis fac
1468	93.5	3.0	490	2	AG1107	internalin G [impo
1469	93.5	3.0	522	2	T36501	probable serine/th
1470	93.5	3.0	530	2	AS3437	poliovirus recepto
1471	93.5	3.0	556	2	T42100	serine/threonine p
1472	93.5	3.0	577	2	T18116	hypothetical prote
1473	93.5	3.0	662	2	T46005	receptor-like prot
1474	93.5	3.0	691	2	B75622	hypothetical prote
1475	93.5	3.0	718	2	T05840	subtilisin-like pr
1476	93.5	3.0	719	2	F96577	protein F12M16.30
1477	93.5	3.0	854	2	A96574	protein F12M16.10
1478	93.5	3.0	909	1	QRXLL2	LDL receptor 2 pre
1479	93.5	3.0	919	2	F83257	hypothetical prote
1480	93.5	3.0	998	2	T35745	probable ATP-bindi
1481	93.5	3.0	1121	2	JC7329	WD-repeat protein
1482	93.5	3.0	2109	2	E89066	protein H05O09.1 [
1483	93.5	3.0	2109	2	T33247	hypothetical prote
1484	93.5	3.0	2150	2	T32497	hypothetical prote
1485	93.5	3.0	2295	2	C88369	protein unc-52 [im
1486	93.5	3.0	3375	2	T19821	hypothetical prote
1487	93	3.0	209	2	T02262	high-methionine d-
1488	93	3.0	221	2	T07079	leucine-rich repea
1489	93	3.0	235	2	PC2022	mucin like protein
1490	93	3.0	328	2	S01359	salivary glue prot
1491	93	3.0	338	2	S38030	suppressor protein
1492	93	3.0	384	2	H70580	hypothetical prote
1493	93	3.0	413	2	AH2743	conserved hypothet
1494	93	3.0	416	2	G97524	hypothetical prote
1495	93	3.0	438	2	G87675	arylesterase-relat
1496	93	3.0	453	2	B42093	serum response fac
1497	93	3.0	465	2	B82515	alpha-L-fucosidase
1498	93	3.0	558	2	T50742	protoporphyrin IX
1499	93	3.0	560	1	JC4795	plasma hyaluronan-
1500	93	3.0	586	2	H86914	conserved hypothet

ALIGNMENTS

RESULT 1
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-lik
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605 <DEL>
A;Cross-references: UNIPARC:UPI00000D50E
C;Comment: This factor is structurally related to proinsulin and have insuline-like meta

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Best Local Similarity   36.2%;  Pred. No. 2e-11;
Matches 100;  Conservative 39;  Mismatches 97;  Indels 40;  Gaps 11;

Qy    7 LILPLILL--LALG--------PGVQG------CPSGCQCSQPQ-----TVFCTARQGTT 45

Db    8 LALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDEVNELSVFCSSRNLTR 67

Qy   46 VPRDVPPDTVGLYVFENGITMLDASSPAGLPGLQLLDLSQNQIASLRLPRLLL------- 98

Db   68 LPDGIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLE-PQALLGLENLCH 126

Qy   99 LDLSHNSLLALEPGILDTANVEALRLAGLG---LQQLDEGLFSRLRNLHDLDVSDNQLER 155

Db  127 LHLERNQLRSLAVGTF--AYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGWNSLAV 184

Qy  156 VP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAAIQELDVSNLSLQALPGDLSGLFPR 214

Db  185 LPDAAFRGLGGLRELVLAGN-RLAYLQPALFSGLAELRELDLSRNALRAIKANVFAQLPR 243

Qy  215 LRLLAAARNPFNCVCPLSWFG---PWVRESHVTLA 246

Db  244 LQKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVA 279
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RESULT 2
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insulin-like growth factor-binding complex acid-labile chain precursor - human
N;Alternate names: Acid-Labile Subunit (ALS)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41915
R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
Mol. Endocrinol. 6, 870-876, 1992
A;Title: Structure and functional expression of the acid-labile subunit of the insulin-1
A;Reference number: A41915; MUID:9257025; PMID:1379671
A;Accession: A41915
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-605 <LEO>

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI00000088A; GB:M86826; NID:g184807; PIDN:
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F;75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
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F;123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F;315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Query Match   9.6%; Score 302; DB 2; Length 605;
Best Local Similarity 35.5%;
Matches 98; Conservative 40; Mismatches 40; Indels 98; Gaps 11;

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Db    8 LALALLLLSWVALGPRSLEGADPGTPGEAEGPACPAACVCSYDDDADELSVFCSSRNLTR 67

Qy   46 VPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLL-------- 98
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Db   68 LPDGVPGTQALWLDGNNLSSVPPAAFQNLSSLGFLNLQGGQLGSLE-PQALLGLENLCH 126

Qy   99 LDLSHNSLLALEPGILDTANVEALRLAGLG---LQQLDEGLFSRLRNLHDLDVSDNQLER 155
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Db  127 LHLERNQIRSLALGTF--AHTPALASLGLSNNRLSRLEDGLFEGLSGSIWDLNLGWNSLAV 184

Qy  156 VP-PVIRLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPR 214
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Qy  215 LRLLAAARNPFNCVCPLSWFG----PWVRESHVTLA 246
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Db  244 LQKLYLDRNLIRAVAPGAFLGLKALRWLDLSHNRVA 279
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RESULT 3
NBHUIA
platelet glycoprotein Ib alpha chain precursor - human
N;Alternate names: membrane glycoprotein Ib alpha chain
N;Contains: glycocalicin
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987
A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p
A;Reference number: A94174; MUID:87289655; PMID:3303030
A;Accession: A94174
A;Molecule type: mRNA
A;Residues: 1-626 <LOP>
A;Cross-references: UNIPROT:P07359; UNIPARC:UPI000012B962; GB:J02940; NID:g183499; PIDN:
R;Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Clemetson, K.J
Thromb. Haemost. 61, 448-453, 1989
A;Title: Isolation and characterization of human blood platelet mRNA and construction of
d cloning of a GPIb coding cDNA insert.
A;Reference number: A60435; MUID:90020160; PMID:2799758
A;Accession: A60435
A;Molecule type: mRNA
A;Residues: 207-467 <WIC>
A;Cross-references: UNIPARC:UPI0000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5514, 1987
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet memb
A;Reference number: A94173; MUID:87289654; PMID:3497398
A;Accession: A94173
A;Molecule type: protein
A;Residues: 17-315 <TIT>
A;Cross-references: UNIPARC:UPI00000174312
R;Hess, D.; Schaller, J.; Rickli, E.B.; Clemetson, K.J.
Eur. J. Biochem. 199, 389-393, 1991
A;Title: Identification of the disulphide bonds in human platelet glycocalicin.
A;Reference number: S16945; MUID:91301149; PMID:2070794
A;Accession: S16945
A;Status: preliminary
A;Molecule type: protein
A;Residues: 224-227;262-270;277-282 <HES>
A;Cross-references: UNIPARC:UPI0000174313; UNIPARC:UPI00000174314; UNIPARC:UPI0000174315
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of ta
ations.
A;Reference number: I55355; MUID:92250564; PMID:1577776
A;Accession: I55355
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 412-427 <RES>
A;Cross-references: UNIPARC:UPI0000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:g
A;Note: variant D
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates
C;Comment: Platelet activation apparently involves disruption of the macromolecular compl
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un
C;Comment: Glycocalicin, which is approximately coextensive with the extracellular part o
C;Genetics:
A;Gene: GDB:GP1BA; GP1B
A;Cross-references: GDB:118806; OMIM:231200
C;Map position: 17pter-17p12
C;Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein re
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repe
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>
F;48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;379-430/Region: proline/threonine-rich 9-residue repeats
F;502-540/Domain: transmembrane #status predicted <TRM>
F;541-626/Domain: intracellular #status predicted <INT>
F;37,175/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match   9.0%; Score 282; DB 1; Length 626;
Best Local Similarity 24.0%; Pred. No. 4.4e-09;
Matches 160; Conservative 72; Mismatches 244; Indels 190; Gaps 26;

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Qy    9 LPILLLALGPGVGVQGCPSGGCQCSQPQT--VFCTARQGTTVPRDVPPDTVGLIVVFEN--- 62
          :||||||  ||||||||||||||||||||    ||||||
Db    1 MPILLLLLLLPSPLHPHPICEVSKVASHLEVNCDKRNLTALPPDLPKDTILHLSENLLY 60

Qy   63 ---------------GITMLDASSF-------AGLPGLQLLDLSQNQIASL-----RLPRLLL 98
                          :| ||  ||          |||||| ||||:||||||      |||||
Db   61 TFSLATLMPYTRLTQLNLDRCELTKLQVDGTLPVLGTLDLSHNQLQSLPLLGQTLPALTV 120

Qy   99 LDLSHNSLLALEPGIL-DTANVEALRLAGLGLGQLQDEGLFSRLRNLHDLDVSDNQLERVP 157
          ||:|:|||||:|  ||  || :| |  :||:|  :||  ||:|| || |:|| :||:||:
Db  121 LDVSFNRLTSLPLGALGLGELQELYLKGNELKTLPPGLLTPTPKLEKLSLANNNLTELP 180

Qy  158 P-VIRLRGLTRLRLAGNTRIAQLRPEDLAGLAGLAGLAALQELDVSNLSLQALPGDLSG--LFPR 214
          . :|  | |: | |:|| |:|  :
Db  181 AGLLNGLENLDTLLLQEN----------------------SLYTIPKGFFGGSHLLPF 215
```

```
Qy  215 LRLLAAARNPFNCVCPLSWFGPWVRES----------------HVTLASPEETRC---------- 253
            ||:|                              ||||: :|
Db  216 AFLHG---NPWLCNCEILYFRRWLQDNAENVYWKQGVDVKAMTSNVASVQCDNSDKPPV 272

Qy  254 -HFPPKNAGRLLLE--LDYADFGCPATTTATVPTTRPVVREP------------TA 295
            ||||                                            ||
Db  273 YKYPGKGCPTLGDEGDTDLYDYYPEEDTEGDKVRATRTVVKFPTKAHTTPWGLFYSWSTA 332

Qy  296 LSSSLAPTWLSPTAPATE-------------------APSPPSTAPPTVGPV---PQ 330
            :|                                   :: ||
Db  333 SLDSQMPSSLHPTQESTKEQTTFPPRWTPNFTLHMESITFSKTPKSTTEPTPSPTTSEPV 392

Qy  331 PQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCSQMGQGTRPSPTPVTPRPPRSLT 390
                                                       |||
Db  393 PEPAPNWTTLEPTP---------SPTTPE-------PTSBPAPSPTTPEPTPIPT 431

Qy  391 LGIEP---VSPTSLRVGLQRYLQGSS--VQLRSLRLTYRNLSGPDKRIVTLR--LPASLA 443
            :|      |||:                     || |
Db  432 IATSPTILVSATSLITPKSTFLTTTKPVSLLESTKKTIPELDQPPKLRGVLQGHLESSRN 491

Qy  444 EYTVTQLRPNATYSVCVMPLG-------------------PGRV-PEGBEACGEAHT 480
                                                    |||||
Db  492 D---PFLHPD---FCCLLLPLGFVVLGLFWLLFASVVLILLLSWVGHVKPQALDSGQGAAL 545

Qy  481 PPAVHSNHAPVTQAREGNLP---LLI---APALAAVLLAALAAVGAAYCVRRGRAMAAA 533
            :|                     :||                       ||
Db  546 TTATQTTHLELQRGRQVTVPRAWLLFLRGSLPTFRSSLFLWVRPNGRVGPLVAGRRPSAL 605

Qy  534 AQDKGQ 539
            :| ||
Db  606 SQGRGQ 611
```

RESULT 4
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1282
R;Dai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A;Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A;Reference number: JC1282; MUID:93038676; PMID:1384485
A;Accession: JC1282
A;Molecule type: mRNA
A;Residues: 1-603 <DAI>
A;Cross-references: UNIPROT:P35859; UNIPARC:UPI0000125918; GB:S46785; NID:g258002; PIDN:
A;Experimental source: liver
A;Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F;267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 9.0%; Score 281.5; DB 2; Length 603;
Best Local Similarity 32.4%; Pred. No. 4.5e-09;
Matches 92; Conservative 49; Mismatches 106; Indels 37; Gaps 11;

```
Qy    6 PLILLPLLLL-LALGP-GVQG-------------------CPSGCQCSQPQ-----TVFCTARQGTT 45
            |||||| |||| :||                       |||| |||
Db    8 PALVLLLAFWVALGPCHLQGGTDPGASADAEGPQCPVACTCSHDDYTDELSVFCSSKNLTH 67

Qy   46 VPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDLSQNOIASLR-----LPRLLLL 99
            :|: ||| |||||:|| || |||| |||
Db   68 LPDDIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLEPAQALLGLQNLYYL 127

Qy  100 DLSHNSLLALEPGIL-DTANVEALRLAGLGLGLQQLDEGLFSRLRLNLHDLVSDNQLERVP- 157
            |:: :|| :: ||  |  ||
Db  128 HLERNLLRNLAVGLFTHTPSLASLSLSSNLLGRLEEGLFQGLSHLWDLNLGWNSLVVLPD 187

Qy  158 PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRL 217
            :| :| || | |||||  | || ||||| | ||:
Db  188 TVFQGLGNLHEIVLAGN-KLTYLQPALFCGLGELRELDLSRNALRSVKANVFVHLPRLQK 246
```

```
Qy  218 LAAAARNPFNCVCPLSWFG----PWRESHVTLAS-PEETRCHFP 256
            ||||                  |||:| :|
Db  247 LYLDRNLITAVAPGAFLGMKALRWLDLSHNRVAGLMEDT---FP 287
```

RESULT 5
JC6128
insulin-like growth factor binding complex acid labile chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6128
R;Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A;Title: Organization and chromosomal localization of the gene encoding the mouse acid 1
A;Reference number: JC6128; MUID:96413591; PMID:8816745
A;Accession: JC6128
A;Molecule type: DNA
A;Residues: 1-603 <BOI>
A;Cross-references: UNIPROT:P70389; UNIPARC:UPI0000000891; GB:U66900; NID:g1621612; PIDN:
C;Comment: This protein is a serum protein and it is of the ternary complex in the physi
C;Genetics:
A;Gene: als
A;Map position: 17

Query Match 8.9%; Score 278.5; DB 2; Length 603;
Best Local Similarity 32.8%; Pred. No. 6.7e-09;
Matches 90; Conservative 48; Mismatches 101; Indels 35; Gaps 10;

```
Qy    6 PLLLPLLLL-LALGP-GVQG-------------------CPSGCQCSQPQ-----TVFCTARQGTT 45
            |||||| |||| :||                      |||| |||
Db    8 PALVLLLAFWVALGPCYLQGTDPGASADAEGPQCPVTCTCSYDDYTDELSVFCSSRNLTQ 67

Qy   46 VPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLL------ 98
            :|: ||| |||||:|| || |||| |||
Db   68 LPDGIPVSTRALWLDGNNLSSIPSAAFQNLSSLDFLNLQGSWLRSLE-PQALLGLQNLYH 126

Qy   99 LDLSHNSLLALEPGIL-DTANVEALRLAGLGLGLQQLDEGLFSRLRLNLHDLDVSDNQLERVP 157
            |:: :|| :: ||  |  ||
Db  127 LHLERNLLRSLAAGLFRHTPSLASLSLSGNNLLGRLEEGLFRGLSHLWDLNLGWNSLVVLP 186

Qy  158 -PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR 216
            :| :| || | |||||  | || ||||| | ||:
Db  187 DTVFQGLGNLHEIVLAGN-KLTYLQPALLCGLGELRELDLSRNALRSVKANVFIHLPRLQ 245

Qy  217 LLAAAARNPFNCVCPLSWFG----PWRESHVTLA 246
            :||||                  |||:| :|
Db  246 KLYLDRNLITAVAPRAFLGMKALRWLDLSHNRVA 279
```

RESULT 6
T42218
slit-1 protein homolog - rat
N;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs t
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:O88279; UNIPARC:UPI000004F20B; EMBL:AB011530; NID:g3449289;
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 8.9%; Score 278; DB 2; Length 1531;
Best Local Similarity 25.8%; Pred. No. 2.1e-08;

Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;

Qy   6 PLLLPLLLLALGPGVQGCPSGCQCPSGCQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT   65

Db   16 PELWLLLWAAAWRLGATACPALCTCI-GTTVDCHGTGLQAIPKNIPRNTERLELNGNNIT   74

Qy   66 MLDASSFAGLPGLQLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGIL-DTANVEALRL   124

Db   75 RIHKNDFAGLKQLRVLQLMENQIG---------AVERGAFPDMKELERLRL   116

Qy   125 AGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPE   183

Db   117 NRNQLQVLPELLFQNNQALSRLDLSENSLQAVPRKAFRGATDLKNLQLDKN-QISCIEEG   175

Qy   184 DLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPNCVCPLSWFGPWVRESHV   243

Db   176 AFRALRGLEVLTLNNNNITTIPVSSFNHMPKLRTFRLHSNHLFCDCHLAWLSQWLRQ-RP   234

Qy   244 TLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPT   303

Db   235 TIGL--FTQCSGPASLRGLNVAEVQKSEFSCSGGQEAAQVPA--------CTLSSGSCPA   284

Qy   304 WLSPTAPATEAPSPPSTAPPTVGPVPQPQ-----------DCPPSTCLNGGTCHLG----   348

Db   285 MCSCSNGIVDCRGKGLTAIPANLPETMTEIRLELNGITIKSIPP----------GAFSPYR   333

Qy   349 ------------TRHHIACLCPEGFTGLYCESQMGGQTRPSPTPVTPRPPRSLTLGIEPVS--PT   399

Db   334 KLRRIDLSNNQIAEIAPDAFQGL-----------------RSLNSLVLIYGNKITDLPR   374

Qy   400 SLRVGLQRYLQGSSVQLRSLRLTYRNLSGPD--KRLVTLRLPA------SLAEYIVTQL   450

Db   375 GVFGGLY------TLQLLLNANKINCIRPDAFQDLQNLSLLSLYDNKIQSLAKGTPFTSL   428

Qy   451 RPNATYSVCVMP   462

Db   429 RAIQTLHLAQNP   440

RESULT 7
A53531
oncofetal trophoblast glycoprotein 5T4 precursor - human
N;Alternate names: oncofetal antigen 5T4
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A53531; S40087
R;Myers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.
J. Biol. Chem. 269, 9319-9324, 1994
A;Title: Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen
A;Reference number: A53531; MUID:94179356; PMID:8132670
A;Accession: A53531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-420 <MEY>
A;Cross-references: UNIPROT:Q13641; UNIPARC:UPI000004CAD5; EMBL:Z29083; NID:g435654; PID
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-420/Product: oncofetal trophoblast glycoprotein 5T4 #status predicted <MAT>

Query Match   8.4%; Score 264.5; DB 2; Length 420;
Best Local Similarity 28.1%; Pred. No. 2.9e-08;
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;

Qy   2 CSRVP-----LLLPLLLLALG-----------PGVQGCPS   26

Db   5 CSRGPAAGDGRLRLARLALVLLGWVSSSPTSSASSFSSASAPPLASAVSAQPPLPDQCPA   64

Qy   27 GCQCSQ-PQTVFCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFAGLP---GLQLLD   82

Db   65 LCECSEAARTVKCVNRNLTEVPTDLPAYVRNLFLTGNQLAVLPAGAFARRPPLAELAALN   124

Qy   83 LSQNQIASLR------LPRLLLLDLSHNSLLALEPGILDTANVEALRLAGLGLQQLDEGL   136

Column 2:

Db   125 LSGSRLDEVRAGAFEHLPSLRLQDLSHNPLADLSPFAFSGSNASV---------SAPSPL   175

Qy   137 FSRLRNLHDLDVSDNQLER------VPPVI-RGLRGLTRLRLAGNTRIAQLRPEDLAGL   188

Db   176 VELILN-HIVPEDERQNRSFPGMVVAALLAGRALQGLRRLRLASN-HFLYLPRDVLAQL   233

Qy   189 AALQELDVSNLSLQALP-----------------GDLSGLFPRLRLLAA   220

Db   234 PSLRHLDLSNNSLVSLLTYVSFRNLTHLESLHLEDNALKVLHNGTLAELQGL-PHIRVF-L   291

Qy   221 ARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGC----PA   276

Db   292 DNNPWVCDCHMADMVTWLKETEV-VQGKDRLTCAYPEKMRNRVLLELNSADLDCDPIIPP   350

Qy   277 TTTTATV   283

Db   351 SLQTSYV   357

RESULT 8
T13953
MEGF5 protein - rat
N;Alternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13953
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs k
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13953
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1523 <NAK>
A;Cross-references: UNIPROT:O88280; UNIPARC:UPI00000E5F7A; EMBL:AB011531; NID:g3449291; I
C;Genetics:
A;Gene: MEGF5
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re

Query Match   8.3%; Score 261; DB 2; Length 1523;
Best Local Similarity 26.3%; Pred. No. 2e-07;
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;

Qy   24 CPSGCQCPSGCQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDL   83

Db   725 CPEQCTCVB-TVVRCSNRGLHTLPKGMPKDVTELYLEGNHLTAV-------------------   767

Qy   84 SQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVEALRLAGLAGLGLQQLDEGLFSRLRNL   143

Db   768 -PKELSTFR--QLTLIDLSNNS----------------------ISMLTNHTFSNMSHL   801

Qy   144 HDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQ   202

Db   802 STILSYNRLRCIPVHAFNGLRSLRVLTILHGN-------------DISSVPEGSFNDLTSLS--   850

Qy   203 ALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGR   262

Db   851 --------HLALGINPLHCDCSLRWLSEWIKAGY--KEPGIARCSSPESMADR   893

Qy   263 LLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAP   322

Db   894 LLLTTPTHRFQCKG-------PVDINIVAKCNACLSS--PCKNNGTCSQDPVBQYRCTCP   944

Qy   323 PTVGPVPQPQDC-PPSTCL---NGGTCHLGTRHH-LACLCPEGFTGLYCE   367

Db   945 YSY---KGKDCTVPINICVQNPCQHGGTCHLSESHRDGFSCSCPLGFEGQRCE   994

RESULT 9
B36665
slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and co
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: B36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
A;Cross-references: UNIPARC:UPI0000177454; GB:X53959
C;Genetics:
A;Gene: FlyBase:sli
A;Cross-references: FlyBase:FBgn0003425
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match   8.1%;   Score 255.5; DB 2; Length 1469;
Best Local Similarity 21.4%; Pred. No. 3.9e-07;
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;

Qy   24 CPSGCCQCSQPQTVFCTARQGTTVPRDVP------------------------PDTVGLY 58
            || |||| || :|| :   :|: |
Db 519 CPAMCHC-EGTTVDCTGRRLKEIPRDIPLHTTELLLNDNELGRISSDGLFGRLPHLVKLE 577

Qy   59 VFENGITMLDASSFAGLPGLQLDLSONQIAS------LRLPRLLLLDLSHNSLLALEPG 112
         | || ||: : || ||| :| |: |:| |||||||||:|| |||
Db 578 LKRNQLTGIEPNAFEGASHIQELQLGBNKIKEISNRKMFLGLHQLKTLNLYDNQISCVMPG 637

Qy 113 ILDTAN------------------------VEALRLAGLGLQQLDEGLFSRLRNLHDLDV-- 148
         :|:|| | ::|:|
Db 638 SFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHS 697

Qy 149 --------------------SDNQLERVP---PV------------------------ 159
                             | |:|||| ||
Db 698 EFKCSSENSEGCLGDGYCPPSCTCTGTVVACSRNQLKEIPRGIPAETSELYLESNEIEQI 757

Qy 160 ---IRGLRGLTRLAGNTRIAQLRPEDLAGLAALQELDVS------------'-NL 199
            |||| ||||| : | :||
Db 758 HYERIRHLRSLTRLDLLS-NNQTILSNYTFANLTKLSTLIISYNKLQCLQRHALSGLNNL 816

Qy 200 SLQALPGDLSGLFPR------------LRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEET 251
         :| :| ||| ||| ||| |||:||| ||||::|| |:|:|
Db 817 RVVSLHGNRISMLPEGSFEDLKSLTHIALGSNPLYCDCGLKWFSDWIKLDYV---EPGIA 873

Qy 252 RCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAPA 311
         || :| : |: | :|||
Db 874 RCAEPEQMKDKJILSTPSSSFVCRGRVRNDILAKCNACFEQPCQNOAQCV------ALPQ 927

Qy 312 TEAPSPPSTAPPTVGPVPQP-------QDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
                               || || :||| |
Db 928 REYQC---------LCQPGYHGKCEFMIDACYGNPCRNNATCTVLEEGRFSCQCAPG 976

Qy 361 FTGLYCESQM 370
         :|||| : :
Db 977 YTGARCETNI 986

RESULT 10
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and co
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: A36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:g8614; PIDN:CAA37910.1; PID:g8
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A;Reference number: A31640; MUID:89077533; PMID:3144436
A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1182,'G',1185-1404,'GT',1463-1464,'YHA' <RO2>
A;Cross-references: UNIPARC:UPI00016BD7A; GB:M23543; NID:g340939; PID:g514357
C;Genetics:
A;Gene: FlyBase:sli
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
C;Keywords: alternative splicing; growth factor
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F;791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match   8.1%;   Score 255.5; DB 2; Length 1480;
Best Local Similarity 21.4%; Pred. No. 4e-07;
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;

Qy   119 VEALRLAGLGLQQLD--------------------------EGLFSRLRNLHDLDVSDNQLERVPP-VIR 161
                ||::| |:||||:| |::::| :.|||||||||||| |||
Db   190 NNILRISESGFQHLENLACLYLGSNNLTKVPSNAFEVLKSLRRLSLSHNPIEAIQPFAFK 249

Qy   162 GLRGLTRLRLAGNTRIAQLRPEDLAGLAAALQELDVSNLSLQALPGD----------------------- 207
                ||||||||||||||||||||||||||||||||||||||||||||||
Db   250 GLANLEYL-LLKQNSRIRNVTRDCFSGINNLKHLILSHNDLENLNSDTFSLLKNLIYLKLD 308

Qy   113 ILDTAN----------------------VEALRLAGLGLQQLDEGLFSRLRNLHDLDV--- 148
                ||||| :| | :|| |:|||| ||| :| ::
Db   638 SFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHS 697

Qy   149 ---------------------SDNQLERVP----------------------PV------ 159
                                     :|||||| ||
Db   149 ---------------------------SDNQLERVP---------------------PV------ 159

Qy   233 WFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVRE 292
                || ||:| || :| | ||||||||||||||||||||||||| | ||||| ::
Db   369 GLRDWLASSAITL----NIYCQNPPSMRGRALRYINITN-----CVTSSINVSRAWAVVKS 420

Qy   293 P-------TAL----------------W-LSPTAPA 311
                                          | |||||
Db   421 PHIHHKTTALMMAWHKVTTNGSPLENTETENITFWERIPTSPA 463

RESULT 12

NBHUA2

Query Match   7.8%; Score 243.5; DB 1; Length 312;
Best Local Similarity 27.5%; Pred. No. 3.4e-07;
Matches   89; Conservative 36; Mismatches 94; Indels 105; Gaps   9;

Qy   25 PSGCQ----------------CSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFA 73
                                    |::||:||||:|:|.| |||:|||||:|||: |
Db   5 PKDCQVFRSDHGSSISCQPP----------------ABIPGYLPADTVHLAVEFFNLTHLPANLLQ 54

Qy   74 GLPGLQLLDLSQNQIASLR---------------LPRLLLLLDLSHNSLLALEPGI------LDTANVEA 121
                || ||||||||:|||:|| |||||||||||||||:||||| |||||:|
Db   55 GASKLQELHLSSNGLESLSPEFLRPVPQLRVDLTRNALTGLPPLFQASATLDTVLVKRE 114

Qy   122 ------------------------LRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPP-VIR 161
                                        ||||||||||||||||||||||||||||||| |||
Db   115 NQLEVLEVSWLHGLKALGHLDLSGNRLRKLPGLLANFTLLRTLDLGENQLETLPPDLLR 174

Qy   162 GLRGLTRLRLAGN------------------------------TRIAQLRPEDLAGLAALQELDVSN 198
                |||||||||:|| |::||||||||||||
Db   175 GPIQLQERLHLEGNKLQVLGKDLLLPQPDLRYLFLNGNKLARVAAGAFQCLRQLDMLDLSN 234

RESULT 11

JC7973

Query Match   8.0%; Score 251; DB 2; Length 622;
Best Local Similarity 23.1%; Pred. No. 2.7e-07;
Matches 107; Conservative 52; Mismatches 142; Indels 162; Gaps   13;

Qy   24 CPSGCQCSQPQTVFCTARQGTTVPRDVP----------------------PDTVGLY 58
                ||: | | |||||||| ||:||| |||||||
Db   519 CPAMCHC-EGTVVDCTGRRLKEIPRDIPLHTTELLNDNELGRISSDGLFGRLPHLVKLE 577

Qy   59 VFENGITMLDASSFAGLPGLQLLDLSQNQIAS-----------------LRLPRLLLLLDLSHNSLLALEPG 112
                || |||||||||||||||||||||:||||| |||||||||||||||||||||
Db   578 LKRNQLTGIEPNAFEGASHIQELQLGENKIKEISNKMFLGLHQLKTLNLYDNQISCVMPG 637

Qy   113 ILDTAN----------------------VEALRLAGLGLQQLDEGLFSRLRNLHDLDV--- 148
                ||||| :| | :|| |:|||| ||| :| ::
Db   638 SFEHLNSLTSLNLASNPFNCNCHLAWFAECVRKKSLNGGAARCGAPSKVRDVQIKDLPHS 697

Qy   149 ---------------------SDNQLERVP----------------------PV------ 159
                                     :|||||| ||
Db   698 EFKCSSENSEGCLGDGYCPPSCTCGTVVACSRNQLKEIPRGIPAETSELYLESNEIEQI 757

Qy   160 ---IRGLRGLTRLRLAGNTRIAQLRPEDLAGLAAALQELDVS--------------NL 199
                   | ||||||||||||||||||||||||||||||||:::
Db   758 HYERIRHLRSLTRLDLS-NNQTTILSNYTFANLTKLSTLIISYNKLQCLQRHALSGLNNL 816

Qy   200 SLQALPGDLSGLFPR--------LRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEET 251
                :|||| | |:|||| |||||||||||||||||| | ||||||||||||||
Db   817 RVVSLHGNRISMLPEGSFEDLKSLTHIALGSNPLYCDCGLKWFSDWIKLDYV---EPGIA 873

Qy   252 RCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAPA 311
                |||||||||||||||||||||||||||:|||||||||||
Db   874 RCAEPEQMKDLKLILSTPSSSFVCRGRVRNDIILAKCNACFEQPCQNQACQV-----ALPQ 927

Qy   312 TEAPSPPSTAPPTVGPVPQP------------------QDCPFSTCLNGGTCHLGTRHHLACLCPEG 360
                | | | | ||||| || |||| ||| |||| | | ||||||
Db   928 REYQC--------------LCQPGVHGKHCEFMIDACYGNPCRNNATCTVLEEGRFSCQCAPG 976

Qy   361 FTGLYCESQM 370
                || | |||
Db   977 YTGARCETNI 986

A;Gene: GDB:GP5
A;Cross-references: GDB:230236; OMIM:173511
A;Map position: 5pter-5qter
C;Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot

Query Match   7.7%; Score 240; DB 2; Length 560;
Best Local Similarity   27.2%; Pred. No. 1e-06;
Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;

Qy   57 LYVFENGITMLDASSFAGLPGLQLLDLSQNQI----ASL-RLPRLLLLDLSHNSLLALE 110
Db 127 LFLDHNALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLP 186

Qy 111 PGILDT-ANVEALRLAGLGLQQLDEGL-------------FSRLRNLHD 145
Db 187 KGLLGAQAKLERILLHSNRIVSLDSGLLNSLGALTELQFHRNHIRSIAPGAFDRLPNLSS 246

Qy 146 LDVS---------------------------------DNQLERVPPVIRG------ 162
Db 247 LTLSRNHLAFLPSALFLHSHNLTLTLFENPLAELPGVLFGEMGGLQELWLNRTQLRTLP 306

Qy 163 --LRGLTRLRLAGNT---RIAQLRPEDLAGLAALQELDV------------------ 196
Db 307 AAAFRNLSRLRYLGVTLSPRLSALPQGAFQGLGELQVLALHSNGLTALPDGLLRGLGKLR 366

Qy 197 ------------------SNLS--------------LQALPGDLSGLFPRLRLLAAARNPFNCV 228
Db 367 QVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETLPGDVFGALPRLTEVLLGHNSWRCD 426

Qy 229 CPLSWFGPWVRESHVTLASPEE-TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTR 287
Db 427 CGLGPFLGWLRQ-HLGLVGGEPPRCAGPAHAGLPLWALPLGGDABCPG--------PRGP 478

Qy 288 PVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGP 327
Db 479 P--PRPAADSSS-----------------EAPVHPALAPNSSEP 503

Qy 199 LSLQALPG----------DLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRES 241
Db 235 NSLASVPEGLWASLGQPNWDMRDGFDISG--------NPWICDQNLSDLYRWLQAQ 282

Qy 242 HVTLASPETRCHFPPKNAGRLLL 265
Db 283 KDRMFSQNDTRCAGPEAVKGQTLL 306

RESULT 13
A60164
platelet membrane glycoprotein V precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Jan-1993 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
R;Lanza, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T
J. Biol. Chem. 268, 20801-20807, 1993
A;Title: Cloning and characterization of the gene encoding the human platelet glycoprote
A;Reference number: A48030; MUID:94012616; PMID:8407908
A;Accession: A48030
A;Molecule type: DNA
A;Residues: 1-560 <LA2>
A;Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:g312501; PID
R;Shimomura, T.; Fujimura, K.; Maehama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama,
Blood 75, 2349-2356, 1990
A;Title: Rapid purification and characterization of human platelet glycoprotein V: the a
A;Reference number, A60164; MUID:90275263; PMID:2350580
A;Accession: A60164
A;Molecule type: protein
A;Residues: 365-384,'X',386-390,'X',392-395,'X',397,188-208,'I',210,27-50,'X',52-53;174-
'XX',108,'T',61-72,'TK',75-77,'V',56-57,'G',479-487,'X',489-498,'X',500,'X',502-503,'X'
2FD; UNIPARC:UPI000017C2FE; UNIPARC:UPI000017C2FF; UNIPARC:UPI000017C300; UNIPARC:UPI000
R;Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.
Biochem. Biophys. Res. Commun. 170, 153-161, 1990
A;Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a
A;Reference number: A35483; MUID:90321220; PMID:2372284
A;Accession: A35483
A;Molecule type: protein
A;Residues: 145-166,'I',168-169,'X',171-172 <ROT>
A;Cross-references: UNIPARC:UPI000017C303
A;Note: this proteolytic fragment was designated peptide M392
A;Accession: B35483
A;Molecule type: Protein
A;Residues: 121-129,'W',131-135,466-468,'X',470 <RO2>
A;Cross-references: UNIPARC:UPI000017C304; UNIPARC:UPI000017C305
A;Note: this material was designated peptide M393 but may contain two peptides
A;Accession: C35483
A;Molecule type: protein
A;Residues: 252-266,'H',268-272,'X',274-279,'I',281-284,'I',286 <RO3>
A;Cross-references: UNIPARC:UPI000017C306; UNIPARC:UPI000017C307
A;Note: this proteolytic fragment was designated peptide M401
R;Zafar, R.S.; Walz, D.A.
Thromb. Res. 53, 31-44, 1989
A;Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl
A;Reference number: A60432; MUID:89162331; PMID:2922700
A;Accession: A60432
A;Molecule type: protein
A;Residues: 477-478,'FX',481-485,'E',487,'V',489-492,'NQ',495,'E',497-498 <ZAF>
A;Cross-references: UNIPARC:UPI000017C307
R;Hickey, M.J.; Hagen, F.S.; Yagi, M.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993
A;Title: Human platelet glycoprotein V: characterization of the polypeptide and the rela
A;Reference number: A47507; MUID:93391348; PMID:7690959
A;Accession: A47507
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-560 <RES>
A;Cross-references: UNIPARC:UPI000004B117; GB:L11238; NID:g388759; PIDN:AAA03069.1; PID
C;Comment: This platelet membrane protein is a substrate for thrombin.
C;Comment: The amino end of the intact protein is blocked.
C;Comment: This protein is absent in Bernard-Soulier syndrome.
C;Genetics:

RESULT 14
JC7763
neuronal leucine-rich repeat protein-3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
R;Fukamachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.
Biochem. Biophys. Res. Commun. 287, 257-263, 2001
A;Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene
A;Reference number: JC7763; PMID:11549284
A;Contents: Fibrosarcoma cells
A;Accession: JC7763
A;Molecule type: mRNA
A;Residues: 1-707 <FUK>
A;Cross-references: UNIPROT:Q9ESY6; UNIPARC:UPI000004F0F2; GB:AF291437
C;Comment: This protein, a new member of the neuronal leucine-rich repeat protein family
in protein-protein interaction and functions as a cell adhesion molecule or soluble liga
C;Genetics:
A;Gene: nlrr-3
C;Keywords: cell adhesion

Query Match   7.6%; Score 237; DB 2; Length 707;
Best Local Similarity   20.7%; Pred. No. 2e-06;
Matches 127; Conservative 80; Mismatches 222; Indels 186; Gaps 22;

Qy   6 PLLLPLLLLALGPGVQG-----------CPSGCQCS----------QPQTVFCTARQGTTVP 47
Db   5 PLQIHVLLGLAITALVQAGDKKVDCPQLCTCEIRPWFTPRSIYMEASTVDCNDLGLLNFP 64

Qy   48 RDVPPPDTVGLYVFENGITMLDASSFAGLP-GLQLLDLSQNQIASL----- 91
Db   65 ARLPADTQILLQTNNIARIEHST--DFPVNLTGLDLSQNNLSSVTNINVQKMSQLLSVY 122

Qy   92 --------RLPRLLLLDLS--------HNSLLALEPGIL------ 114

```
Db   123 LEENKLTELPEKCLYGLSNLQELYVNNLLSAISPGAFVGLINLLRHLNSNRLQMINSK 182         Db   338 ----EGAFNDLSA----LSHLAIGANPLYCDCNMQWLSDWVKSEY---KEPGIARCAGPG 386

Qy   115 ---DTANVEALRL----------------------AGLGLQQLDEGLFSRLRNLHDLD 147         Qy   258 KNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLLAPTWLSPTAPATEAPSP 317
         ||:||                           : :||||     |||: :  |||           : :|||      |   :                      ||: :  |||
Db   183 WFEALPNLEILMLGDNPILRIKDMNFQPLLKLRSLVIAGINLJTEVPDDALVGLENLESIS 242         Db   387 EMADKLLLTTPSKKFTCQ---------------------------GPMDITIQAKCNPCLSN 421

Qy   148 VSDNQLERVP---------------------PVIRGLRG----------------- 165         Qy   318 PSTAPPTVGPVP-----------QPQDCP-----PSTCLNGGTCHL--GTRHHLACL 356
         ||:|:||                        : ||                               |||                 :  ||||  |  ||||||||:|
Db   243 FYDNRLNKVPQVALQKAVNLKFIDLNKNPINRIRRGDFSNMLHLKELGINNMPELVSIDS 302         Db   422 PCKNDGTCNNDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCHLKEGENAGFWCT 481

Qy   166 ------LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQAL-PGDLSGLFPRLR 216         Qy   357 CPEGFTGLYCE 367
         :   :::|:| :||                 |: :| || :  |  :| : |||          | :|||| ||
Db   303 LAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESL-PNLK 361         Db   482 CADGFEGENCE 492

Qy   217 LLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPA 276

Db   362 EISIHSNPIRCDCVIRWIN--MNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDM---- 415         Search completed: January   5, 2006, 13:54:15
                                                                                  Job time : 43 secs
Qy   277 TTTTATVPTTRPVVREPTALSSSL---APTWLSPTAPATEAPSPPSTAPPTVGPVPQPQD 333
         :    | |:   :|:|| : :   :   |||||
Db   416 -----MEICLPLI-APESFPSILDVEADSVVSLHCRATAEFQ-----PEIYWITPSGKR 463

Qy   334 CPPSTCLNGGTCHL-GTRHHLACLCPEGFTGLY---CESQMGQGTRPSPTPVTPRPR-- 387
         |:|             :   ||||| |   ||        |||  |   : ||
Db   464 LLPNTLREKFVVHSEGTLDIRGITPKEG--GLYTCIATNLVGADLKSIMIKVGGFVPQDN 521

Qy   388 --SLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY 445
              | |||    |  |:| |        |: : ||  :|||  |:|| ||
Db   522 NGSLNIKIRDIRANSVLVS---WKANSKILKSSVKWTAFVKTEDSQAAQSARIPSDVKVY 578

Qy   446 TVTQLRPNATYSVCV 460
            : |||  : :|:|
Db   579 NLTHLKPSTEYKICI 593


RESULT 15
T42626
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
N;Alternate names: neurogenic extracellular slit protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42626
R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H.
Mech. Dev. 79, 57-72, 1998
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in
A;Reference number: Z22177; MUID:99279238; PMID:10349621
A;Accession: T42626
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1025 <HOL>
A;Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI00000E8104; EMBL:AF074960; NID:g4151258;
C;Genetics:
A;Gene: Slit2
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match             7.4%;  Score 231;  DB 2;  Length 1025;
Best Local Similarity  24.0%;  Pred. No. 6.9e-06;
Matches   89;  Conservative  32;  Mismatches 122;  Indels 128;  Gaps   13;

Qy    24 CPSGCGCQSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGITMLDASSFAGLPGLQLLDL 83
         |:| |   |:|  :|          | ||  |  |   ::|| ||        ||| |||:|
Db   223 CPSECTCLD-TXVRCSNKGLKVLPKGIPKDVTELYLDCNQFTLIV-PKELSNVKHLTLIDL 280

Qy    84 SONQIASL------RLPRLLLDLSHNSLLALEPGILDTANVEALRLAGLGLQQLDEGLF 137
         |:|:|||       ::|::||: ||  | |                  |||||||||||
Db   281 SNNRISTLSNQXFSNMTQLLTLILSYNRLRCIPPRTFD----------GLKSL---- 323

Qy   138 SRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS 197
          ||| |||||| :|:|| ||  |:|  | ||| :||||||||||||||||||||||||||
Db   324 -RLLSLHGNDIS------VVP----------------------------------- 337

Qy   198 NLSLQALPGDLSGLFPRLRLAAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPP 257
         ||||   ||||| || |||:                |:| ||  |||  :   ::
Db   257
```

OM protein - protein search, using sw model

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            Copyright (c) 1993 - 2006 Compugen Ltd.

Run on: January 5, 2006, 13:49:48 ; Search time 229 Seconds
                                         (without alignments)
                                         1842.384 Million cell updates/sec

Title: US-09-943-780-69
Perfect score: 3135
Sequence: 1 MCSRVPLLPLLLLLALGPG..........PLMGPPGPGLQSPLHAKPYI 598

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 216443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1500 summaries

Database :   UniProt_05.80:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                    SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3135	100.0	598	2	Q6UXL5_HUMAN	Q6uxl5 homo sapien
2	3083.5	98.4	673	2	Q6UXL4_HUMAN	Q6uxl4 homo sapien
3	3078.5	98.2	673	2	Q6EMK4_HUMAN	Q6emk4 homo sapien
4	2697.5	86.0	601	2	Q96CX1_HUMAN	Q96cx1 homo sapien
5	2491	79.5	673	2	Q8BJJ0_MOUSE	Q8bjj0 m mus muscu
6	2490	79.4	673	2	Q8R2G5_MOUSE	Q8r2g5 mus musculu
7	2484	79.2	673	2	Q9CZT5_MOUSE	Q9czt5 m mus muscu
8	1213.5	38.7	661	2	Q6DF55_XENTR	Q6df55 xenopus tro
9	927.5	29.6	643	2	Q503G2_BRARE	Q503g2 brachydanio
10	914.5	29.2	962	2	Q4SQ68_TETNG	Q4sq68 tetraodon n
11	368.5	11.8	513	2	Q50IG9_HUMAN	Q50ig9 homo sapien
12	359.5	11.5	635	1	LRFN4_HUMAN	Q6pjg9 homo sapien
13	351	11.2	636	1	LRFN4_MOUSE	Q80xu8 mus musculu
14	341	10.9	660	2	Q8BLU0_MOUSE	Q8blu0 mus musculu
15	339	10.8	521	2	Q8BHA1_MOUSE	Q8bha1 m mus muscu
16	338	10.8	655	2	Q4SGV9_TETNG	Q4sgv9 tetraodon n
17	333	10.6	858	2	Q5TYT7_BRARE	Q5tyt7 brachydanio
18	332	10.6	637	2	Q6A073_MOUSE	Q6a073 mus musculu
19	331.5	10.6	622	2	Q59GV4_HUMAN	Q59gv4 homo sapien
20	330	10.5	653	1	LRRC4_HUMAN	Q9hbw1 homo sapien
21	329.5	10.5	648	2	Q6DDY0_XENLA	Q6ddy0 xenopus lae
22	325.5	10.4	570	2	Q70AK2_XENLA	Q70ak2 xenopus lae
23	324	10.3	626	1	LRFN3_MOUSE	Q8bly3 mus musculu
24	324	10.3	626	2	Q505E2_MOUSE	Q505e2 mus musculu
25	323	10.3	732	2	Q4RPB8_TETNG	Q4rpb8 tetraodon n
26	322.5	10.3	682	2	Q6DJD2_XENLA	Q6djd2 xenopus lae
27	322.5	10.3	811	2	Q7L0X0_HUMAN	Q7l0x0 homo sapien
28	322.5	10.3	887	2	O75139_HUMAN	O75139 homo sapien
29	322	10.3	605	1	ALS_PAPHA	002833 papio hamad
30	321	10.2	628	1	LRFN3_HUMAN	Q9btn0 homo sapien
31	321	10.2	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
32	320	10.2	660	1	FLRT2_HUMAN	O43155 homo sapien
33	320	10.2	674	2	Q6RKD8_MOUSE	Q6rkd8 mus musculu
34	319	10.2	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
35	318.5	10.1	652	1	LRRC4_MOUSE	Q99ph1 mus musculu
36	317	10.1	778	1	Q6NUI6_HUMAN	Q6nui6 homo sapien
37	312.5	10.0	648	2	Q70AK3_XENLA	Q70ak3 xenopus lae
38	312.5	10.0	935	2	Q4BT7_TETNG	Q4bt7 tetraodon n
39	311.5	9.9	420	2	Q7M6Z0_MOUSE	Q7m6z0 mus musculu
40	310.5	9.9	420	2	Q80WD1_RAT	Q80wd1 rattus norv
41	310.5	9.9	646	1	FLRT1_HUMAN	Q9nzu1 homo sapien
42	308	9.8	627	2	Q8NC95_HUMAN	Q8nc95 homo sapien
43	308	9.8	649	1	FLRT3_HUMAN	Q9nzu0 homo sapien
44	308	9.8	649	2	Q542Z9_HUMAN	Q542z9 homo sapien
45	307.5	9.8	626	1	Q4TBM8_TETNG	Q4tbm8 tetraodon n
46	307.5	9.8	674	2	Q8WVA2_HUMAN	Q8wva2 homo sapien
47	307	9.8	637	2	Q68F21_XENLA	Q68f21 xenopus lae
48	307	9.8	649	2	Q5R6T0_PONPY	Q5r6t0 pongo pygma
49	306.5	9.8	730	2	Q6PHP6_MOUSE	Q6php6 mus musculu
50	305.5	9.7	692	2	Q6US92_MOUSE	Q6us92 mus musculu
51	303.5	9.6	420	2	Q4G0S0_HUMAN	Q4g0s0 homo sapien
52	302.5	9.6	420	2	Q6X813_HUMAN	Q6x813 homo sapien
53	302.5	9.6	420	1	Q86UN3_HUMAN	Q86un3 homo sapien
54	302.5	9.6	618	2	Q4SHD7_TETNG	Q4shd7 tetraodon n
55	302	9.6	605	1	ALS1_HUMAN	P35858 homo sapien
56	302	9.6	605	2	Q8TAY0_HUMAN	Q8tay0 homo sapien
57	299.5	9.6	677	2	Q28256_CANFA	Q28256 canis famil
58	298.5	9.5	649	2	Q8BGT1_MOUSE	Q8bgt1 mus musculu
59	298.5	9.5	663	2	Q62PQ1_MOUSE	Q62pq1 mus musculu
60	295.5	9.4	640	1	NGL1_MOUSE	Q8c031 mus musculu
61	295.5	9.4	640	2	Q50SE5_MOUSE	Q50se5 mus musculu
62	294.5	9.4	647	2	Q50SI7_BRARE	Q50si7 brachydanio
63	293.5	9.3	809	2	Q9DBY4_MOUSE	Q9dby4 m mus muscu
64	292.5	9.3	640	2	NGL1_HUMAN	Q9hcj2 homo sapien
65	292.5	9.3	837	2	Q80TV0_MOUSE	Q80tv0 mus musculu
66	288.5	9.2	372	2	Q72W3_BRARE	Q72w3 brachydanio
67	288.5	9.2	581	2	Q4SYI7_TETNG	Q4syi7 tetraodon n
68	288.5	9.2	640	2	Q4JIW0_HUMAN	Q4jiw0 homo sapien
69	287.5	9.2	428	2	Q4S4W6_TETNG	Q4s4w6 tetraodon n
70	287.5	9.2	713	1	LRRN5_HUMAN	O75325 homo sapien
71	286	9.1	650	2	Q4RQ15_TETNG	Q4rq15 tetraodon n
72	285	9.1	640	2	Q4JIV9_HUMAN	Q4jiv9 homo sapien
73	284.5	9.1	457	2	Q6WZD1_BRARE	Q6wzd1 brachydanio
74	284	9.1	782	2	Q5TOV4_HUMAN	Q5t0v4 homo sapien
75	283.5	9.0	603	2	O70211_RAT	O70211 rattus norv
76	283	9.0	1515	2	Q9D837_BRARE	Q9de37 brachydanio
77	282.5	9.0	745	2	Q6UKK2_HUMAN	Q6uxk2 homo sapien
78	282.5	9.0	785	2	Q9P263_HUMAN	Q9p263 homo sapien
79	282	9.0	626	1	GP1BA_HUMAN	P07359 homo sapien
80	281.5	9.0	603	1	ALS_RAT	P35859 rattus norv
81	281	8.9	738	2	Q90Z45_CHICK	Q90z45 gallus gall
82	280	8.9	633	2	Q4SR95_TETNG	Q4sr95 tetraodon n
83	279.5	8.9	619	2	Q570Z9_MOUSE	Q570z9 mus musculu
84	278.5	8.9	603	1	ALS_MOUSE	P70389 mus musculu
85	278.5	8.9	603	2	Q799IQ5_MOUSE	Q799iQ5 mus musculu
86	278.5	8.9	687	2	Q9JIL0_MOUSE	Q9jil0 mus musculu
87	278	8.9	321	2	Q6E4K4_PETMA	Q6e4k4 petromyzon
88	278	8.8	1531	1	SLIT1_RAT	O88279 rattus norv
89	277	8.8	330	2	Q4G1K9_EPTBU	Q4g1k9 eptatretus
90	276	8.8	1071	2	Q4RTI6_TETNG	Q4rti6 tetraodon n
91	276	8.8	1531	1	SLIT1_MOUSE	Q80tr4 mus musculu
92	276	8.8	2623	2	Q6WRI0_HUMAN	Q6wri0 homo sapien
93	273.5	8.7	593	2	Q6UY18_HUMAN	Q6uy18 homo sapien
94	273.5	8.7	1504	1	SLIT_DROME	P24014 drosophila
95	273	8.7	745	2	Q5RKR3_MOUSE	Q5rkr3 mus musculu
96	273	8.7	785	2	Q62PQ3_MOUSE	Q62pq3 mus musculu
97	271.5	8.7	342	2	Q91XL1_MOUSE	Q91xl1 mus musculu
98	271.5	8.7	1312	2	Q61PF0_CAEBR	Q61pf0 caenorhabdi
99	271	8.6	473	1	RTN4R_HUMAN	Q9bzr6 homo sapien
100	271	8.6	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc
101	270.5	8.6	541	2	Q6PK41_HUMAN	Q6pk41 homo sapien
102	270	8.6	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
103	270	8.6	1461	2	Q5VW18_HUMAN	Q5vw18 homo sapien
104	270	8.6	1534	1	SLIT1_HUMAN	O75093 homo sapien

#	Score	Score2	Length	N	Name	Accession	Organism
105	270	8.6	1534	2	Q5VW17_HUMAN	Q5vw17	homo sapien
106	268.5	8.6	409	2	Q5T0V2_HUMAN	Q5t0v2	homo sapien
107	268	8.5	417	2	Q6E4J7_PETMA	Q6e4j7	petromyzon
108	267.5	8.5	1512	2	Q9DE36_BRARE	Q9de36	brachydanio
109	266.5	8.5	1529	2	Q7ZXI2_XENLA	Q7zxi2	xenopus lae
110	266	8.5	460	2	Q6IPL6_HUMAN	Q6ipl6	homo sapien
111	266	8.5	734	2	035930_MOUSE	035930	mus musculu
112	265.5	8.5	1044	2	Q5ISR9_MACFA	Q5isr9	macaca fasc
113	265	8.5	298	2	Q4GL17_EPTBU	Q4gl17	eptatretus
114	265	8.5	734	2	Q5SX47_MOUSE	Q5sx47	mus musculu
115	264.5	8.4	420	1	TPBG_HUMAN	Q13641	homo sapien
116	264	8.4	334	2	Q5VSG2_HUMAN	Q5vsg2	homo sapien
117	264	8.4	352	2	Q4GL11_EPTBU	Q4gl11	eptatretus
118	263	8.4	332	2	Q5I0E1_RAT	Q5i0e1	rattus norv
119	263	8.4	1253	2	Q4T0S1_TETNG	Q4t0s1	tetraodon n
120	262	8.4	346	2	Q4GL19_EPTBU	Q4gl19	eptatretus
121	261.5	8.3	347	1	AGL_HUMAN	P02750	homo sapien
122	261	8.3	321	1	Q6E4D1_PETMA	Q6e4d1	petromyzon
123	258	8.2	1523	1	SLIT3_HUMAN	075094	homo sapien
124	258	8.2	324	2	Q4S3K9_TETNG	Q4s3k9	tetraodon n
125	257.5	8.2	501	2	Q4SZC5_TETNG	Q4szc5	tetraodon n
126	257.5	8.2	473	1	RTN4R_RAT	Q99m75	rattus norv
127	257	8.2	739	2	Q8BKM5_MOUSE	Q8bkm5	mus musculu
128	257	8.2	342	2	Q4SGG5_TETNG	Q4sgg5	tetraodon n
129	256.5	8.1	1095	2	Q90XG4_CHICK	Q90xg4	gallus gall
130	255.5	8.1	528	2	Q8N644_HUMAN	Q8n644	homo sapien
131	254	8.1	1523	1	SLIT3_MOUSE	Q9wvb4	mus musculu
132	254	8.1	1523	2	Q5SS56_MOUSE	Q5ss56	mus musculu
133	254	8.1	347	2	Q68CK4_HUMAN	Q68ck4	homo sapien
134	253.5	8.1	589	2	Q6GQU6_MOUSE	Q6gqu6	mus musculu
135	253.5	8.1	1410	2	Q20204_CAEEL	Q20204	caenorhabdi
136	253.5	8.1	426	1	TPBG_MOUSE	Q9z010	mus musculu
137	253	8.1	567	2	GPV_MOUSE	008742	mus musculu
138	253	8.1	311	2	Q6E4L1_PETMA	Q6e411	petromyzon
139	252	8.0	426	1	TPBG_RAT	Q5pqv5	rattus norv
140	252	8.0	567	2	Q9ZU3_MOUSE	Q9zu3	mus musculu
141	252	8.0	473	1	RTN4R_MOUSE	Q99pi8	mus musculu
142	251	8.0	542	2	Q9N4G6_CAEEL	Q9n4g6	caenorhabdi
143	251	8.0	622	2	Q6ZWI5_HUMAN	Q6zwi5	homo sapien
144	251	8.0	622	2	Q7Z2Q7_HUMAN	Q7z2q7	homo sapien
145	251	8.0	1021	2	Q9V430_DROME	Q9v430	drosophila
146	250	8.0	412	2	Q4RRU8_TETNG	Q4rru8	tetraodon n
147	249.5	8.0	789	1	LRFN2_HUMAN	Q9ulh4	homo sapien
148	249.5	8.0	789	1	LRFN2_MACFA	Q9be71	macaca fasc
149	249.5	8.0	420	2	Q6WRH9_RAT	Q6wrh9	rattus norv
150	248.5	7.9	481	1	TPBG_MACFA	Q4r8y9	macaca fasc
151	248.5	7.9	481	1	NYX_HUMAN	Q9gzu5	homo sapien
152	248	7.9	305	2	Q5H983_HUMAN	Q5h983	homo sapien
153	248	7.9	1521	2	Q4GL13_EPTBU	Q4gl13	eptatretus
154	247.5	7.9	1529	1	SLIT2_MOUSE	Q9r1b9	mus musculu
155	247.5	7.9	794	1	SLIT2_HUMAN	094813	homo sapien
156	247.5	7.9	331	2	Q90WZ3_XENLA	Q90wz3	xenopus lae
157	247.5	7.8	308	2	Q4SK16_TETNG	Q4sk16	tetraodon n
158	247	7.8	544	2	Q4GL13_EPTST	Q4gl13	eptatretus
159	246	7.8	306	2	Q91W20_MOUSE	Q91w20	mus musculu
160	245.5	7.8	321	2	Q1X58_CAEBR	Q1x58	caenorhabdi
161	245.5	7.8	708	2	Q4GLK6_EPTST	Q4gl1k6	eptatretus
162	245	7.8	708	2	Q6E4J9_PETMA	Q6e4j9	petromyzon
163	245	7.8	411	2	Q8IYQ6_HUMAN	Q8iyq6	homo sapien
164	245	7.8	718	2	Q5R482_PONPY	Q5r482	pongo pygma
165	245	7.8	766	2	Q4S6L6_TETNG	Q4s6l6	tetraodon n
166	244.5	7.8	788	2	073675_XENLA	073675	xenopus lae
167	244.5	7.8	1593	1	SLIT2_RAT	Q9wvc1	rattus norv
168	244.5	7.8	458	1	LRFN2_MOUSE	Q80tg9	mus musculu
169	244.5	7.8	567	2	Q5DTL5_MOUSE	Q5dt15	mus musculu
170	244.5	7.8	708	2	Q6WZD3_BRARE	Q6wzd3	brachydanio
171	244	7.8	567	1	GPV_RAT	008770	rattus norv
172	244	7.8	708	2	Q9H3W5_HUMAN	Q9h3w5	homo sapien
173	243.5	7.8	476	1	NYX_MOUSE	P83503	mus musculu
174	243	7.8	321	2	Q6E4L4_PETMA	Q6e414	petromyzon
175	243	7.8	708	2	Q6I9V8_HUMAN	Q6i9v8	homo sapien
176	243	7.8	388	2	Q6ZM54_BRARE	Q6zm54	brachydanio
177	242.5	7.7					
178	242.5	7.7	545	1	CPN2_HUMAN	P22792	homo sapien
179	242.5	7.7	718	2	Q6PCK4_XENLA	Q6pck4	xenopus lae
180	242	7.7	380	2	Q5T0V3_HUMAN	Q5t0v3	homo sapien
181	242	7.7	652	2	Q7PVZ3_ANOGA	Q7pvz3	anopheles g
182	241.5	7.7	272	2	Q4KP12_LAMAP	Q4kp12	lampetra ap
183	241.5	7.7	311	2	Q4E4L3_PETMA	Q6e413	petromyzon
184	240	7.6	560	1	GPV_HUMAN	P40197	homo sapien
185	239.5	7.6	370	2	Q8BGX3_MOUSE	Q8bgx3	m mus muscu
186	239.5	7.6	786	2	Q5TU01_ANOGA	Q5tu01	anopheles g
187	239.5	7.6	1256	2	Q7QCT2_ANOGA	Q7qct2	anopheles g
188	238	7.6	323	2	Q4KP13_9PETR	Q4kp13	ichthyomyzo
189	238	7.6	453	2	Q86XY1_HUMAN	Q86xy1	homo sapien
190	238	7.6	544	2	Q8UV23_9PERC	Q8uv23	sphoeroides
191	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9d3k0	m mus muscu
192	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4s4c0	tetraodon n
193	237	7.6	289	2	Q4KP06_LAMAP	Q4kp06	lampetra ap
194	237	7.6	370	2	Q8N967_HUMAN	Q8n967	homo sapien
195	237	7.6	578	1	LRC15_RAT	Q9r5m3	rattus norv
196	237	7.6	707	1	Q9ESY6_RAT	Q9esy6	rattus norv
197	237	7.6	1046	2	Q7PZJ7_ANOGA	Q7pzj7	anopheles g
198	236.5	7.5	461	2	Q4SA12_TETNG	Q4sa12	tetraodon n
199	236.5	7.5	715	2	Q4RY04_TETNG	Q4ry04	tetraodon n
200	236	7.5	707	2	Q8CBC6_MOUSE	Q8cbc6	mus musculu
201	236	7.5	718	2	Q6P6Z7_XENLA	Q6p6z7	xenopus lae
202	235.5	7.5	296	1	Q4GLH6_EPTST	Q4glh6	eptatretus
203	235.5	7.5	579	1	LRC15_MOUSE	Q80x72	mus musculu
204	235	7.5	574	2	Q4RRR5_TETNG	Q4rrr5	tetraodon n
205	234.5	7.5	488	2	Q4RK86_TETNG	Q4rk86	tetraodon n
206	234	7.5	707	2	P97860_MOUSE	P97860	mus musculu
207	233.5	7.4	298	2	Q6E4J4_PETMA	Q6e4j4	petromyzon
208	233.5	7.4	545	2	Q4SW26_TETNG	Q4sw26	tetraodon n
209	233	7.4	1316	2	Q9VQ25_DROME	Q9vq25	drosophila
210	232	7.4	487	2	Q4SA13_TETNG	Q4sa13	tetraodon n
211	231.5	7.4	283	1	Q4GLH4_EPTST	Q4glh4	eptatretus
212	231.5	7.4	840	1	SLIK6_MOUSE	08c110	mus musculu
213	231	7.4	294	2	Q5VT99_HUMAN	Q5vt99	homo sapien
214	231	7.4	547	1	CPN2_MOUSE	09dbb9	mus musculu
215	231	7.4	619	2	Q7QBW2_ANOGA	Q7qbw2	anopheles g
216	231	7.4	707	2	Q642E4_RAT	0642e4	rattus norv
217	231	7.4	787	2	Q4SCX3_TETNG	Q4scx3	tetraodon n
218	230.5	7.3	332	2	Q8QFN6_ELAQU	Q8qfn6	elaphe quad
219	230	7.3	332	2	Q8QFN7_ELAQU	Q8qfn7	elaphe quad
220	230	7.3	872	2	Q4SZ04_TETNG	Q4sz04	tetraodon n
221	230	7.3	1229	2	Q4T7S0_TETNG	Q4t7s0	tetraodon n
222	230	7.3	828	2	Q8C8T7_MOUSE	Q8c8t7	mus musculu
223	229	7.3	581	1	LRC15_HUMAN	Q8tf66	homo sapien
224	228.5	7.3	294	2	Q6E4L6_PETMA	Q6e416	petromyzon
225	228.5	7.3	341	2	Q6ZSA7_HUMAN	Q6zsa7	homo sapien
226	228.5	7.3	342	2	Q4RRU5_TETNG	Q4rru5	tetraodon n
227	228.5	7.3	310	2	Q4RRQ4_TETNG	Q4rrq4	tetraodon n
228	228	7.3	838	2	Q4SPP9_TETNG	Q4spp9	tetraodon n
229	228	7.3	356	2	Q8BXQ3_MOUSE	Q8bxq3	m mus muscu
230	227.5	7.2	326	2	Q4KLL3_RAT	Q4kll3	rattus norv
231	227	7.2	783	2	Q90XG2_CHICK	Q90xg2	gallus gall
232	227	7.2	950	2	Q90Z44_CHICK	Q90z44	gallus gall
233	227	7.2	283	2	Q4GLI1_EPTST	Q4gli1	eptatretus
234	226.5	7.2	298	2	Q4KP15_9PETR	Q4kp15	ichthyomyzo
235	226.5	7.2	299	2	Q4GLI9_EPTST	Q4gli9	eptatretus
236	226.5	7.2	557	1	LG11_HUMAN	095970	homo sapien
237	226.5	7.2	719	1	LRFN5_HUMAN	Q9ni6	homo sapien
238	226	7.2	321	2	Q4KP16_9PETR	Q4kp16	ichthyomyzo
239	226	7.2	364	2	Q4SQ63_TETNG	Q4sq63	tetraodon n
240	226	7.2	210	2	Q4SCF1_TETNG	Q4scf1	tetraodon n
241	225.5	7.1	298	2	Q6E4J3_PETMA	Q6e4j3	petromyzon
242	225.5	7.1	283	2	Q4GLH8_EPTST	Q4glh8	eptatretus
243	223.5	7.1	647	2	Q4SLN0_TETNG	Q4sln0	tetraodon n
244	223.5	7.1	289	2	Q4SIN0_TETNG	Q4sin0	tetraodon n
245	223	7.1	349	2	Q6E4C8_PETMA	Q6e4c8	petromyzon
246	223	7.1	413	2	Q4SH52_TETNG	Q4sh52	tetraodon n
247	222.5	7.1	557	2	Q64ZI5_9PETR	Q64zi5	mus musculu
248	222.5	7.1	557	1	GLI1_RAT	P83503	rattus norv
249	222.5	7.1	557	2	Q5R945_PONPY	Q5r945	pongo pygma
250	222.5	7.1	557	2	Q5FW57_RAT	Q5fw57	rattus norv

No.	Length	pI	Score	ID	Accession	Species
251	792	7.1	222.5	Q90Z43_CHICK	Q90z43	gallus gall
252	269	7.1	222	Q6E4L0_PETMA	Q6e410	petromyzon
253	348	7.1	222	Q95J8_MACFA	Q95j8	macaca fasc
254	722	7.1	222	Q5PPU2_XENLA	Q5ppu2	xenopus lae
255	475	7.1	221.5	Q4T109_TETNG	Q4t109	tetraodon n
256	557	7.1	221.5	LG11_MOUSE	Q9jla1	mus musculu
257	719	7.1	221.5	LRFN5_MOUSE	Q8bxa0	mus musculu
258	721	7.0	221	LRIG1_MOUSE	Q5dth4	mus musculu
259	1093	7.0	221	LRIG1_HUMAN	Q96ja1	homo sapien
260	210	7.0	220.5	Q6E4M1_PETMA	Q6e4m1	petromyzon
261	306	7.0	220.5	Q4KP04_LAMAP	Q4kp04	lampetra ap
262	322	7.0	220.5	Q6E4K1_PETMA	Q6e4k1	petromyzon
263	342	7.0	220.5	Q4RW94_TETNG	Q4rw94	tetraodon n
264	515	7.0	220.5	LRTM2_MOUSE	Q8bga3	mus musculu
265	515	7.0	220.5	Q8C8L1_MOUSE	Q8c8l1	mus musculu
266	733	7.0	220.5	Q24250_DROME	Q24250	drosophila
267	841	7.0	220.5	SLIK6_HUMAN	Q9h5y7	homo sapien
268	582	7.0	220	LRTM3_MOUSE	Q8bz81	mus musculu
269	582	7.0	220	Q8BZA0_MOUSE	Q8bza0	mus musculu
270	603	7.0	220	Q4SJ27_TETNG	Q4sj27	tetraodon n
271	583	7.0	220	Q4SNQ0_TETNG	Q4snq0	tetraodon n
272	334	7.0	219	Q6P7C4_RAT	Q6p7c4	rattus norv
273	359	7.0	218.5	Q6GTU0_HUMAN	Q6gtu0	homo sapien
274	618	7.0	218.5	LRC21_MOUSE	Q8k099	mus musculu
275	288	6.9	217.5	Q8BR15_MOUSE	Q8br15	mus musculu
276	615	6.9	217.5	Q4SLS7_TETNG	Q4sls7	tetraodon n
277	695	6.9	217.5	Q4TLY8_TETNG	Q4tly8	tetraodon n
278	1335	6.9	217.5	Q610C7_CAEBR	Q610c7	caenorhabdi
279	637	6.9	217	Q6DCV7_XENLA	Q6dcv7	xenopus lae
280	263	6.9	216	Q6E4C7_PETMA	Q6e4c7	petromyzon
281	282	6.9	216	Q4G1I6_EPTST	Q4g1i6	eptatretus
282	514	6.9	216	Q4VBX1_MOUSE	Q4vbx1	mus musculu
283	329	6.9	215.5	Q56NG5_CIOIN	Q56ng5	ciona intes
284	331	6.9	215.5	PLIB_AGKBL	O93233	agkistrodon
285	612	6.9	215.5	Q4SYK9_TETNG	Q4syk9	tetraodon n
286	737	6.9	215	Q9VU51_DROME	Q9vu51	drosophila
287	743	6.8	215	Q6P1M7_HUMAN	Q6p1m7	homo sapien
288	329	6.8	215	Q56NG6_CIOIN	Q56ng6	ciona intes
289	441	6.8	215	Q86UN2_HUMAN	Q86un2	homo sapien
290	716	6.8	214.5	LRRN1_HUMAN	Q6uxks	homo sapien
291	731	6.8	214.5	Q4T149_TETNG	Q4t149	tetraodon n
292	1535	6.8	214.5	Q23991_DROME	Q23991	drosophila
293	295	6.8	214.5	Q6E4C9_PETMA	Q6e4c9	petromyzon
294	516	6.8	214	LRTM2_HUMAN	O43300	homo sapien
295	717	6.8	214	Q4SR34_TETNG	Q4sr34	tetraodon n
296	2828	6.8	214	Q9NR99_HUMAN	Q9nr99	homo sapien
297	238	6.7	213.5	Q6E4J5_PETMA	Q6e4j5	petromyzon
298	273	6.7	213.5	Q4G1L2_EPTBU	Q4g1l2	eptatretus
299	359	6.7	213.5	CHAD_HUMAN	O15335	homo sapien
300	361	6.7	213.5	CHAD_BOVIN	Q27972	bos taurus
301	438	6.7	213	Q7TQ96_RAT	Q7tq96	rattus norv
302	716	6.7	213	LRRN1_MOUSE	Q61809	mus musculu
303	604	6.7	212.5	Q4SHE8_TETNG	Q4she8	tetraodon n
304	276	6.7	212	Q4G1J9_EPTST	Q4g1j9	eptatretus
305	445	6.7	212	Q80WD0_RAT	Q80wd0	rattus norv
306	918	6.7	212	Q7Q3F0_ANOGA	Q7q3f0	anopheles g
307	192	6.7	211.5	Q6E4I9_PETMA	Q6e4i9	petromyzon
308	270	6.7	211.5	Q6E4L7_PETMA	Q6e4l7	petromyzon
309	518	6.7	211.5	Q5R712_PONPY	Q5r712	pongo pygma
310	187	6.7	211	Q6E4I2_PETMA	Q6e4i2	petromyzon
311	581	6.7	211	LRTM3_HUMAN	Q86vh5	homo sapien
312	581	6.7	211	LRTM3_MACFA	Q4g1m3	macaca fasc
313	257	6.7	210.5	Q4G1M3_EPTBU	Q4g1m3	eptatretus
314	321	6.7	210.5	Q6E4L5_PETMA	Q6e4l5	petromyzon
315	4303	6.7	210.5	PKD1_HUMAN	P98161	homo_sapien
316	358	6.7	210	CHAD_RAT	O70210	rattus norv
317	1028	6.7	210	Q865R7_PIG	Q865r7	sus scrofa
318	214	6.7	209.5	Q6E4H0_PETMA	Q6e4h0	petromyzon
319	533	6.7	209.5	Q5E9T6_BOVIN	Q5e9t6	bos taurus
320	211	6.7	209	Q6E4I3_PETMA	Q6e4i3	petromyzon
321	257	6.7	209	Q6E4J6_PETMA	Q6e4j6	petromyzon
322	353	6.7	209	Q6UXK1_HUMAN	Q6uxk1	homo sapien
323	358	6.7	209	CHAD_MOUSE	O55226	mus musculu

No.	ID	Cnt	Length	pI	Score	Accession	Species
324	Q5SUV4_MOUSE	2	358	6.7	209	Q5suv4	mus musculu
325	Q4S8B7_TETNG	2	391	6.7	209	Q4s8b7	tetraodon n
326	LRIG1_MOUSE	2	1091	6.7	209	P70193	mus musculu
327	Q5RH06_BRARE	2	350	6.7	208.5	Q5rh06	brachydanio
328	PRELP_HUMAN	1	382	6.7	208.5	P51888	homo sapien
329	Q6FHG6_HUMAN	2	382	6.7	208.5	Q6fhg6	homo sapien
330	Q6FG38_HUMAN	2	382	6.7	208.5	Q6fg38	homo sapien
331	Q8K0S5_MOUSE	2	445	6.7	208.5	Q8k0s5	m reticulon
332	Q6X3Y5_BRARE	2	479	6.7	208.5	Q6x3y5	brachydanio
333	LRTM4_HUMAN	1	518	6.7	208.5	Q86vh4	homo sapien
334	Q4FZ98_HUMAN	2	518	6.7	208.5	Q4fz98	homo sapien
335	Q4KMX1_HUMAN	2	519	6.7	208.5	Q4kmx1	homo sapien
336	LGI4_HUMAN	1	537	6.7	208.5	Q8n135	homo sapien
337	Q60XJ7_HUMAN	2	590	6.6	208.5	Q6uxj7	homo sapien
338	Q9VK22_DROME	2	649	6.6	208	Q9vk22	drosophila
339	Q6E4F0_PETMA	2	180	6.6	207.5	Q6e4f0	petromyzon
340	Q4S074_TETNG	2	330	6.6	207.5	Q4s074	tetraodon n
341	Q6ZT31_HUMAN	2	518	6.6	207.5	Q6zt31	homo sapien
342	GP124_MOUSE	1	1329	6.6	207.5	Q91zv8	mus musculu
343	Q5T9K5_HUMAN	2	313	6.6	207	Q5t9k5	homo sapien
344	Q8N7C0_HUMAN	2	313	6.6	207	Q8n7c0	homo sapien
345	Q6P0D2_BRARE	2	536	6.6	207	Q6p0d2	brachydanio
346	Q5O144_CHICK	2	613	6.6	207	Q5o144	gallus gall
347	Q5JWV6_HUMAN	2	740	6.6	207	Q5jwv6	homo sapien
348	O08852_MOUSE	2	4293	6.6	207	O08852	mus musculu
349	Q6E4K6_PETMA	2	270	6.6	206.5	Q6e4k6	petromyzon
350	Q6E4B9_PETMA	2	274	6.6	206.5	Q6e4b9	petromyzon
351	Q6E4C1_PETMA	2	274	6.6	206.5	Q6e4c1	petromyzon
352	Q6E4L2_PETMA	2	294	6.6	206.5	Q6e412	petromyzon
353	Q5U4S7_XENLA	2	327	6.6	206.5	Q5u4s7	xenopus lae
354	Q8ND46_HUMAN	2	423	6.6	206.5	Q8nd46	homo sapien
355	Q9D1T0_MOUSE	2	614	6.6	206	Q9d1t0	mus musculu
356	Q9UJX9_HUMAN	2	353	6.6	206	Q9ujx9	homo sapien
357	Q8WUA8_HUMAN	2	353	6.6	206	Q8wua8	homo sapien
358	PRELP_BOVIN	1	381	6.6	206	Q9gkn8	bos taurus
359	O14498	2	428	6.6	206	O14498	homo sapien
360	Q5TPW2_ANOGA	2	539	6.6	206	Q5tpw2	anopheles g
361	Q8BZD4_MOUSE	2	606	6.6	206	Q8bzd4	m mus muscu
362	Q8BLC0_MOUSE	2	606	6.6	206	Q8blc0	m mus muscu
363	Q5U1A7_DROME	2	738	6.6	206	Q5u1a7	drosophila
364	LRIG2_MOUSE	1	1054	6.6	206	Q52kr2	mus musculu
365	Q4TAT9_TETNG	2	1127	6.6	206	Q4tat9	tetraodon n
366	Q6E4H2_PETMA	2	212	6.6	205.5	Q6e4h2	petromyzon
367	Q6DH76_BRARE	2	479	6.6	205.5	Q6dh76	brachydanio
368	Q99KT6_MOUSE	2	492	6.6	205.5	Q99kt6	mus musculu
369	LRTM4_MOUSE	1	590	6.6	205.5	Q80xg9	mus musculu
370	Q4G1K4_EPTST	2	248	6.5	205	Q4g1k4	eptatretus
371	Q4G1L6_EPTST	2	256	6.5	205	Q4g1l6	eptatretus
372	Q4RU74_TETNG	2	486	6.5	205	Q4ru74	tetraodon n
373	Q5RDJ4_PONPY	2	614	6.5	205	Q5rdj4	pongo pygma
374	Q9N008_MACFA	2	614	6.5	205	Q9n008	macaca fasc
375	Q96FE5_HUMAN	2	620	6.5	205	Q96fe5	homo sapien
376	CT075_HUMAN	1	740	6.5	205	Q8c1v9	mus musculu
377	Q6QMY6_RAT	2	353	6.5	204.5	Q6qmy6	rattus norv
378	Q9V7J8_DROME	2	1173	6.5	204	Q9v7j8	drosophila
379	Q6P4S1_XENLA	2	1306	6.5	204	Q6p4s1	xenopus lae
380	Q6AI13_HUMAN	2	845	6.5	203.5	Q6ai13	homo sapien
381	Q9VKG1_DROME	2	894	6.5	203.5	Q9vkg1	drosophila
382	Q53ME4_ORYSA	2	1061	6.5	203.5	Q53me4	oryza sativ
383	LRIG2_HUMAN	1	1065	6.5	203.5	O94898	homo sapien
384	Q6E4B6_PETMA	2	269	6.5	203	Q6e4b6	petromyzon
385	Q5NVQ6_PONPY	2	428	6.5	203	Q5nvq6	pongo pygma
386	Q4R3P6_MACFA	2	602	6.5	203	Q4r3p6	macaca fasc
387	Q4SLZ4_TETNG	2	703	6.5	203	Q4slz4	tetraodon n
388	Q6NN49_DROME	2	740	6.5	203	Q6nn49	drosophila
389	Q9NBK9_DROME	2	1514	6.5	203	Q9nbk9	drosophila
390	Q9VUN0_DROME	2	1514	6.5	203	Q9vun0	drosophila
391	Q4G1K1_EPTST	2	203	6.5	203	Q4g1k1	eptatretus
392	Q4G1H5_EPTST	2	259	6.5	202.5	Q4g1h5	eptatretus
393	Q4RIG0_TETNG	2	259	6.5	202.5	Q4rig0	tetraodon n
394	Q6E4J2_PETMA	2	274	6.5	202.5	Q6e4j2	petromyzon
395	Q4KPL1_LAMAP	2	829	6.5	202.5	Q4kpl1	lampetra ap
396	—	2	271	6.4	202	—	—

Left column block:

No.	Score	E	Len	ID	N	Accession	Species
397	202	6.4	1117	Q5VQM7_ORYSA	2	Q5vqm7	oryza sativ
398	201.5	6.4	187	Q6E4D7_PETMA	2	Q6e4d7	petromyzon
399	201.5	6.4	275	Q4G1J5_EPTST	2	Q4g1j5	eptatretus
400	201.5	6.4	372	Q8CBR6_MOUSE	2	Q8cbr6	mus musculu
401	201.5	6.4	457	Q960D1_DROME	2	Q960d1	drosophila
402	201.5	6.4	524	Q4RG59_TETNG	2	Q4rg59	tetraodon n
403	201.5	6.4	551	Q4RF95_TETNG	2	Q4rf95	tetraodon n
404	201.5	6.4	606	Q9BZ20_HUMAN	2	Q9bz20	homo sapien
405	201.5	6.4	892	P91644_DROME	2	P91644	drosophila
406	201.5	6.4	1527	Q9VZZ4_DROME	2	Q9vzz4	drosophila
407	201	6.4	213	Q6E4H6_PETMA	2	Q6e4h6	petromyzon
408	201	6.4	218	Q6E4K9_PETMA	2	Q6e4k9	petromyzon
409	201	6.4	336	Q48M5_TETNG	2	Q48m5	petromyzon
410	201	6.4	354	Q4W655_MOUSE	2	Q4w655	mus musculu
411	201	6.4	430	Q58F20_HUMAN	2	Q58f20	homo sapien
412	201	6.4	581	Q9BTR7_HUMAN	2	Q9btr7	homo sapien
413	201	6.4	602	Q9H9A6_HUMAN	2	Q9h9a6	homo sapien
414	201	6.4	712	Q5BL20_BRARE	2	Q5bl20	brachydanio
415	200.5	6.4	845	SLIK2_HUMAN	1	Q9h156	homo sapien
416	200	6.4	460	Q4RK03_TETNG	2	Q4rk03	tetraodon n
417	200	6.4	616	Q58A95_CAEEL	2	Q58a95	caenorhabdi
418	200	6.4	653	O02329_CAEEL	2	O02329	caenorhabdi
419	199.5	6.4	227	Q4SP28_TETNG	2	Q4sp28	tetraodon n
420	199.5	6.4	261	Q4G1L4_EPTBU	2	Q4g1l4	eptatretus
421	199.5	6.3	622	Q66HV9_BRARE	2	Q66hv9	brachydanio
422	199	6.3	846	SLIK2_MOUSE	1	Q810c0	mus musculu
423	199	6.3	862	Q4SST3_TETNG	2	Q4sst3	tetraodon n
424	199	6.3	1328	Q21043_CAEEL	2	Q21043	caenorhabdi
425	198.5	6.3	259	Q4G1J4_EPTST	2	Q4g1j4	eptatretus
426	198.5	6.3	320	Q6YN44_HUMAN	2	Q6yn44	homo sapien
427	198.5	6.3	617	LRC21_RAT	1	Q9jmh2	rattus norv
428	198.5	6.3	741	Q4SWG9_TETNG	2	Q4swg9	tetraodon n
429	198.5	6.3	873	Q7XR24_ORYSA	2	Q7xr24	oryza sativ
430	198.5	6.3	1331	GP124_HUMAN	1	Q96pe1	homo sapien
431	198	6.3	363	Q7SYE5_BRARE	2	Q7sye5	brachydanio
432	198	6.3	602	Q5RFE9_PONPY	2	Q5rfe9	pongo pygma
433	197.5	6.3	280	Q6E4K8_PETMA	2	Q6e4k8	petromyzon
434	197.5	6.3	300	Q4VBZ3_HUMAN	2	Q4vbz3	homo sapien
435	197.5	6.3	441	Q9VE49_DROME	2	Q9ve49	drosophila
436	197.5	6.3	537	LGI3_HUMAN	1	Q8n145	homo sapien
437	197.5	6.3	548	Q4R4H3_MACFA	2	Q4r4h3	macaca fasc
438	197.5	6.3	548	Q4SIX2_TETNG	2	Q4six2	tetraodon n
439	197.5	6.3	818	Q4SFB0_TETNG	2	Q4sfb0	tetraodon n
440	197.5	6.3	835	GP125_HUMAN	1	Q8iwk6	homo sapien
441	197.5	6.3	1321	Q9HBL6_HUMAN	2	Q9hbl6	homo sapien
442	197	6.3	345	Q6YXX5_ORYSA	2	Q6yxx5	oryza sativ
443	197	6.3	1093	Q5XWD3_HUMAN	2	Q5xwd3	homo sapien
444	197	6.3	694	Q4G1J3_EPTST	2	Q4g1j3	eptatretus
445	196.5	6.3	837	Q4G1J1_EPTST	2	Q4g1j1	eptatretus
446	196.5	6.3	370	Q6E4D0_PETMA	2	Q6e4d0	petromyzon
447	196	6.3	378	Q15142_HUMAN	2	Q15142	homo sapien
448	196	6.3	378	Q58DI7_BOVIN	2	Q58di7	bos taurus
449	195.5	6.2	917	PRELP_MOUSE	1	Q9jk53	mus musculu
450	195.5	6.2	931	Q543S0_MOUSE	2	Q543s0	mus musculu
451	195.5	6.2	440	Q86PM1_DROME	2	Q86pm1	drosophila
452	195.5	6.2	614	Q9VWI6_DROME	2	Q9vwi6	drosophila
453	195	6.2	620	Q4RSH2_MACFA	2	Q4rsh2	macaca fasc
454	195	6.2	837	Q6NUK3_HUMAN	2	Q6nuk3	homo sapien
455	195	6.2	369	Q60XM3_HUMAN	2	Q6uxm3	homo sapien
456	195	6.2	693	SLIK4_HUMAN	1	Q6iw52	homo sapien
457	195	6.2	699	Q5JXG3_HUMAN	2	Q5jxg3	homo sapien
458	195	6.2	699	Q65Z91_CHICK	2	Q65z91	gallus gall
459	194.5	6.2	737	Q7Z3D0_HUMAN	2	Q7z3d0	homo sapien
460	194.5	6.2	881	ECM2_HUMAN	1	Q94769	homo sapien
461	194.5	6.2	1630	Q5T9F2_HUMAN	2	Q5t9f2	homo sapien
462	194.5	6.2	258	Q965M3_CAEEL	2	Q965m3	caenorhabdi
463	194.5	6.2	258	Q965M2_CAEEL	2	Q965m2	caenorhabdi
464	194.5	6.2	263	LAP4_HUMAN	1	Q14160	homo sapien
465	194.5	6.2	611	Q4G1J0_EPTST	2	Q4g1j0	eptatretus
466	194	6.2	258	Q4G1I0_EPTST	2	Q4g1i0	eptatretus
467	194	6.2	263	Q6E4C0_PETMA	2	Q6e4c0	petromyzon
468	194	6.2	611	Q4RHK3_TETNG	2	Q4rhk3	tetraodon n
469	194	6.2					

Right column block:

No.	Accession	Species	ID	N	Len	E	Score
470	Q4rv46	tetraodon n	Q4RV46_TETNG	2	692	6.2	194
471	Q9v9v6	drosophila	Q9V9V6_DROME	2	836	6.2	194
472	Q6e4h8	petromyzon	Q6E4H8_PETMA	2	186	6.2	193.5
473	Q4kp03	lampetra ap	Q4KP03_LAMAP	2	270	6.2	193.5
474	Q4g1m1	eptatretus	Q4G1M1_EPTBU	2	273	6.2	193.5
475	Q9eqp5	rattus norv	PRELP_RAT	1	377	6.2	193.5
476	Q8caz9	mus musculu	Q8CAZ9_MOUSE	2	378	6.2	193.5
477	Q9nt99	homo sapien	Q9NT99_HUMAN	2	421	6.2	193.5
478	Q6idg7	drosophila	Q6IDG7_DROME	2	433	6.2	193.5
479	Q80v4	homo sapien	LGI2_HUMAN	2	545	6.2	193.5
480	Q60w68	caenorhabdi	Q60W68_CAEBR	2	574	6.2	193.5
481	Q10690	mycobacteri	Y2082_MYCTU	2	721	6.2	193.5
482	Q7tz24	mycobacteri	Q7TZ24_MYCBO	2	721	6.2	193.5
483	Q96c25	homo sapien	Q9C25_HUMAN	2	893	6.2	193.5
484	Q9hb75	homo sapien	Q9HB75_HUMAN	2	910	6.2	193.5
485	Q94933	homo sapien	SLIK3_HUMAN	2	977	6.2	193.5
486	Q4g1i2	eptatretus	Q4G1I2_EPTST	2	252	6.2	193
487	Q4szu8	tetraodon n	Q4SZU8_TETNG	2	497	6.2	193
488	Q9nk84	homo sapien	Q9NK84_HUMAN	2	540	6.2	193
489	Q9vjn8	drosophila	Q9VJN8_DROME	2	550	6.2	193
490	Q6e4d5	petromyzon	Q6E4D5_PETMA	2	187	6.1	192.5
491	Q6e4g0	petromyzon	Q6E4G0_PETMA	2	214	6.1	192.5
492	Q4g1h7	eptatretus	Q4G1H7_EPTST	2	259	6.1	192.5
493	Q6e4k0	petromyzon	Q6E4K0_PETMA	2	270	6.1	192.5
494	Q6gu68	mus musculu	Q6GU68_MOUSE	2	428	6.1	192.5
495	Q50dz7	mus musculu	Q50DZ7_MOUSE	2	542	6.1	192.5
496	Q23580	caenorhabdi	Q23580_CAEEL	2	575	6.1	192.5
497	Q6ha06	crassostrea	Q6HA06_CRAGI	2	1093	6.1	192.5
498	Q6e4k2	petromyzon	Q6E4K2_PETMA	2	265	6.1	192
499	Q6e4c5	petromyzon	Q6E4C5_PETMA	2	273	6.1	192
500	Q8k406	mus musculu	LGI3_MOUSE	2	548	6.1	192
501	Q6un14	leishmania	Q6UN14_LEICH	2	627	6.1	192
502	Q6e4i7	petromyzon	Q6E4I7_PETMA	2	187	6.1	191.5
503	Q6e4j8	petromyzon	Q6E4J8_PETMA	2	204	6.1	191.5
504	Q9erv7	mus musculu	Q9ERV7_MOUSE	2	915	6.1	191.5
505	Q810b9	mus musculu	SLIK3_MOUSE	1	980	6.1	191.5
506	Q6nzm5	mus musculu	Q6NZM5_MOUSE	2	980	6.1	191.5
507	Q4kp00	lampetra ap	Q4KP00_LAMAP	2	271	6.1	191
508	Q5rcq8	pongo pygma	Q5RCQ8_PONPY	2	440	6.1	191
509	Q4t1m0	tetraodon n	Q4T1M0_TETNG	2	610	6.1	191
510	Q4g1i7	eptatretus	Q4G1I7_EPTST	2	251	6.1	190.5
511	Q5h721	fugu rubrip	Q5H721_FUGRU	2	894	6.1	190.5
512	Q6rn19	drosophila	Q6RN19_DROME	2	1238	6.1	190.5
513	Q9vpf0	drosophila	Q9VPF0_DROME	2	1535	6.1	190.5
514	Q6e4h3	petromyzon	Q6E4H3_PETMA	2	191	6.1	190
515	Q4re68	tetraodon n	Q4RE68_TETNG	2	639	6.1	190
516	Q628n6	caenorhabdi	Q628N6_CAEBR	2	654	6.1	190
517	P59383	mus musculu	CTO75_MOUSE	2	733	6.1	190
518	Q6uxm1	homo sapien	LRIG3_HUMAN	2	1119	6.1	190
519	Q9v477	drosophila	Q9V477_DROME	2	1346	6.1	190
520	Q6xhb1	dictyosteli	Q6XHB1_DICDI	2	2800	6.1	190
521	Q4g1j7	eptatretus	Q4G1J7_EPTST	2	252	6.1	189.5
522	Q4rsx9	tetraodon n	Q4RSX9_TETNG	2	370	6.1	189.5
523	P28653	mus musculu	PGS1_MOUSE	1	369	6.0	189
524	P47853	rattus norv	PGS1_RAT	1	369	6.0	189
525	Q4t5r5	tetraodon n	Q4T5R5_TETNG	2	627	6.0	189
526	Q4qgi8	leishmania	Q4QGI8_LBIMA	2	760	6.0	189
527	Q9sn46	arabidopsis	Q9SN46_ARATH	2	839	6.0	189
528	Q9vad1	drosophila	Q9VAD1_DROME	2	1392	6.0	189
529	Q7yqk5	canis famil	Q7YQK5_CANFA	2	4311	6.0	188.5
530	Q6gmi5	brachydanio	Q6GMI5_BRARE	2	369	6.0	188.5
531	Q504e0	brachydanio	Q504E0_BRARE	2	370	6.0	188.5
532	Q9ddz7	petromyzon	Q9DDZ7_PETMA	2	410	6.0	188.5
533	Q5syh5	mus musculu	Q5SYH5_MOUSE	2	433	6.0	188.5
534	Q63912	mus musculu	OMGP_MOUSE	1	440	6.0	188.5
535	Q5z8w0	oryza sativ	Q5Z8W0_ORYSA	2	538	6.0	188.5
536	Q4sbu9	tetraodon n	Q4SBU9_TETNG	2	655	6.0	188.5
537	Q53hu6	homo sapien	Q53HU6_HUMAN	2	368	6.0	188
538	O02678	canis famil	PGS1_CANFA	1	369	6.0	188
539	Q7tmw3	mus musculu	Q7TMW3_MOUSE	2	369	6.0	188
540	Q8k377	mus musculu	LRTM1_MOUSE	1	522	6.0	188
541	Q4se92	tetraodon n	Q4SE92_TETNG	2	626	6.0	188
542	Q5zih8	gallus gall	Q5ZIH8_CHICK	2	818	6.0	188

No.	Length	Value	ID (short)	Accession	Species
543	187.5	6.0	259	Q4G1L0_EPTBU	Q4G1L0 eptatretus
544	187.5	6.0	310	Q9DDZ8_PETMA	Q9ddz8 petromyzon
545	187.5	6.0	350	Q5M7S9_XENTR	Q5m7s9 xenopus tro
546	187.5	6.0	352	Q4W6V7_CHICK	Q4w6v7 gallus gall
547	187.5	6.0	363	Q9H5G9_HUMAN	Q9h5g9 homo sapien
548	187.5	6.0	425	Q9VGH2_DROME	Q9vgh2 drosophila
549	187.5	6.0	601	Q7SXW3_BRARE	Q7sxw3 brachydanio
550	187.5	6.0	861	Q4ZJ82_CHICK	Q4zj82 gallus gall
551	187	6.0	260	Q4G1K7_EPTST	Q4g1k7 eptatretus
552	187	6.0	262	Q4G1K0_EPTST	Q4g1k0 eptatretus
553	187	6.0	592	Q61PG4_CAEBR	Q61pg4 caenorhabdi
554	187	6.0	615	Q9VZ84_DROME	Q9vz84 drosophila
555	187	6.0	735	Q6EI14_MOUSE	Q6ei14 mus musculu
556	187	6.0	818	Q5WA51_CHICK	Q5wa51 gallus gall
557	187	6.0	1741	Q5LJU2_DROME	Q5lju2 drosophila
558	186.5	5.9	368	PGS1_XENLA	Q9ib75 xenopus lae
559	186.5	5.9	521	Q72U34_LEPIC	Q72u34 leptospira
560	186.5	5.9	639	Q5VZI7_HUMAN	Q5vzi7 homo sapien
561	186.5	5.9	799	Q5VZI8_HUMAN	Q5vzi8 homo sapien
562	186.5	5.9	839	TLR4_HUMAN	O00206 homo sapien
563	186.5	5.9	839	TLR4_PANPA	Q9ttn0 pan paniscu
564	186.5	5.9	839	Q5VZI9_HUMAN	Q5vzi9 homo sapien
565	186	5.9	273	Q6E4B4_PETMA	Q6e4b4 petromyzon
566	186	5.9	368	Q5RAY4_PONPY	Q5ray4 pongo pygma
567	186	5.9	440	OMGP_HUMAN	P23515 homo sapien
568	186	5.9	440	Q53HB8_HUMAN	Q53hb8 homo sapien
569	186	5.9	552	Q9VT44_DROME	Q9vt44 drosophila
570	186	5.9	623	LRC21_HUMAN	Q9p2v4 homo sapien
571	186	5.9	1029	Q5I2M5_BOVIN	Q5i2m5 bos taurus
572	185.5	5.9	369	Q4T3M1_TETNG	Q4t3m1 tetraodon n
573	185.5	5.9	466	Q66IW3_XENLA	Q66iw3 xenopus lae
574	185.5	5.9	953	Q6MF87_PARUW	Q6mf87 parachlamyd
575	185	5.9	254	Q4S4N7_TETNG	Q4s4n7 tetraodon n
576	185	5.9	389	Q6PBP5_BRARE	Q6pbp5 brachydanio
577	185	5.9	512	Q6PEZ8_HUMAN	Q6pez8 homo sapien
578	185	5.9	603	Q5ZLN0_CHICK	Q5zln0 gallus gall
579	184.5	5.9	257	Q4G1L5_EPTBU	Q4g1l5 eptatretus
580	184.5	5.9	270	Q4KP09_LAMAP	Q4kp09 lampetra ap
581	184.5	5.9	724	Q5XWB9_HORSE	Q5xwb9 equus cabal
582	184.5	5.9	799	Q9V964_DROME	Q9v964 drosophila
583	184.5	5.9	839	Q69ZV6_MOUSE	Q69zv6 mus musculu
584	184.5	5.9	841	Q5F4K7_PIG	Q5f4k7 sus scrofa
585	184.5	5.9	843	TLR4_HORSE	Q9myw3 equus cabal
586	184.5	5.9	957	SLIK5_MOUSE	Q810b7 mus musculu
587	184.5	5.9	1007	Q65XS3_ORYSA	Q65xs3 oryza sativ
588	184.5	5.9	1046	Q5GQ97_CHICK	Q5gq97 gallus gall
589	184.5	5.9	1214	Q69JN6_ORYSA	Q69jn6 oryza sativ
590	184	5.9	187	Q6E4M5_PETMA	Q6e4m5 petromyzon
591	184	5.9	253	Q6E4K5_PETMA	Q6e4k5 petromyzon
592	184	5.9	263	Q6E4K7_PETMA	Q6e4k7 petromyzon
593	184	5.9	274	Q4G1M0_EPTBU	Q4g1m0 eptatretus
594	184	5.9	291	Q4RF21_TETNG	Q4rf21 tetraodon n
595	184	5.9	368	PGS1_HUMAN	P21810 homo sapien
596	184	5.9	368	Q53FI4_HUMAN	Q53fi4 homo sapien
597	184	5.9	473	Q7QF76_ANOGA	Q7qf76 anopheles g
598	184	5.9	543	Q4RGC6_TETNG	Q4rgc6 tetraodon n
599	184	5.9	552	Q6K6X6_ORYSA	Q6k6x6 oryza sativ
600	184	5.9	565	Q7PJD0_ANOGA	Q7pjd0 anopheles g
601	184	5.9	837	SLIK4_MOUSE	Q810b8 mus musculu
602	183.5	5.9	187	Q6E4F6_PETMA	Q6e4f6 petromyzon
603	183.5	5.9	287	Q9W2B9_DROME	Q9w2b9 drosophila
604	183.5	5.9	292	Q6NYY6_BRARE	Q6nyy6 brachydanio
605	183.5	5.9	601	Q6TLH1_BRARE	Q6tlh1 brachydanio
606	183.5	5.9	652	Q7Q696_ANOGA	Q7q696 anopheles g
607	183.5	5.9	727	Q6A0E8_MOUSE	Q6a0e8 mus musculu
608	183.5	5.9	795	TLR1_MOUSE	Q9epg1 mus musculu
609	183.5	5.9	824	Q5GGX1_PIG	Q5ggx1 sus scrofa
610	183.5	5.9	841	TLR4_PIG	Q68y56 sus scrofa
611	183.5	5.9	1059	Q5ZJD0_CHICK	Q5zjd0 gallus gall
612	183.5	5.9	1495	Q5VXC2_HUMAN	Q5vxc2 homo sapien
613	183.5	5.9	1537	LRRC7_HUMAN	Q96nw7 homo sapien
614	183.5	5.9	1537	Q5VXC3_HUMAN	Q5vxc3 homo sapien
615	183	5.8	540	Q9VU53_DROME	Q9vu53 drosophila
616	183	5.8	568	Q6P3Y9_MOUSE	Q6p3y9 mus musculu
617	183	5.8	662	LRC32_HUMAN	Q14392 homo sapien
618	183	5.8	664	Q72T8I_ONCMY	Q72t8i oncorhynchu
619	183	5.8	972	Q5ZJ34_CHICK	Q5zj34 gallus gall
620	182.5	5.8	187	Q6E4G1_PETMA	Q6e4g1 petromyzon
621	182.5	5.8	187	Q6E4G7_PETMA	Q6e4g7 petromyzon
622	182.5	5.8	257	Q4G1L8_EPTBU	Q4g1l8 eptatretus
623	182.5	5.8	379	ASPN_HUMAN	Q9bxn1 homo sapien
624	182.5	5.8	380	Q5TBF3_HUMAN	Q5tbf3 homo sapien
625	182.5	5.8	384	Q6P528_HUMAN	Q6p528 homo sapien
626	182.5	5.8	810	Q8T3J2_DROME	Q8t3j2 drosophila
627	182.5	5.8	811	Q9VK54_DROME	Q9vk54 drosophila
628	182.5	5.8	828	TLR4_PONPY	Q8pe14 pongo pygma
629	182.5	5.8	837	P91643_DROME	Q8pe9 gorilla gor
630	182.5	5.8	880	SLIK5_HUMAN	P91643 drosophila
631	182.5	5.8	958	Q5VT8I_HUMAN	O94991 homo sapien
632	182.5	5.8	958	Q4QOH1_HUMAN	Q5vt81 homo sapien
633	182.5	5.8	958	Q4R9X7_TETNG	Q4qoh1 homo sapien
634	182	5.8	205	Q4G1I8_EPTST	Q4r9x7 tetraodon n
635	182	5.8	252	Q6E4C4_PETMA	Q4g1i8 eptatretus
636	182	5.8	271	Q4RU73_TETNG	Q6e4c4 petromyzon
637	182	5.8	297	PGS1_SHEEP	Q4ru73 tetraodon n
638	182	5.8	369	Q5BIM3_BOVIN	O46390 ovis aries
639	182	5.8	369	Q803T1_BRARE	Q5bim3 bos taurus
640	182	5.8	373	Q5RI45_BRARE	Q803t1 brachydanio
641	182	5.8	373	Q8F3F8_LEPIN	Q5ri45 brachydanio
642	182	5.8	428	O96671_DROME	Q8f3f8 leptospira
643	182	5.8	532	Q7Q550_ANOGA	O96671 drosophila
644	182	5.8	678	Q8HXV0_BOVIN	Q7q550 anopheles g
645	182	5.8	1022	Q866B2_BOVIN	Q8hxv0 bos taurus
646	182	5.8	1029	Q8BPJ0_MOUSE	Q866b2 bos taurus
647	181.5	5.8	180	Q4G1K2_EPTST	Q8bpj0 mus musculu
648	181.5	5.8	251	Q4G1J8_EPTST	Q4g1k2 eptatretus
649	181.5	5.8	259	PGS2_CHICK	Q4g1j8 eptatretus
650	181.5	5.8	357	Q7T3H6_BRARE	Q7t3h6 brachydanio
651	181.5	5.8	599	Q61PG3_CAEBR	Q61pg3 caenorhabdi
652	181.5	5.8	699	O13328_MAGGR	O13328 magnaporthe
653	181.5	5.8	2160	O13488_MAGGR	O13488 magnaporthe
654	181.5	5.8	2160	Q51J05_MAGGR	Q51j05 magnaporthe
655	181.5	5.8	2160	PGS1_HORSE	O46403 equus cabal
656	181	5.8	372	Q7QIP3_ANOGA	Q7qip3 anopheles g
657	181	5.8	569	Q8LQ10_ORYSA	Q8lq10 oryza sativ
658	181	5.8	1013	Q7QI68_ANOGA	Q7qi68 anopheles g
659	181	5.8	1333	Q6GLQ6_XENLA	Q6glq6 xenopus lae
660	180.5	5.8	371	Q8BMW6_MOUSE	Q8bmw6 mus musculu
661	180.5	5.8	385	Q8I170_DROVI	Q8i170 drosophila
662	180.5	5.8	441	AMGO2_PONPY	Q69jn6 mus musculu
663	180.5	5.8	522	Q6PGX3_BRARE	Q5r7m3 ponpy
664	180.5	5.8	584	Q96PY3_HUMAN	Q6pgx3 brachydanio
665	180.5	5.8	821	Q9VJQ0_DROME	Q96py3 homo sapien
666	180.5	5.8	1443	Q5HZ61_XENTR	Q9vjq0 drosophila
667	180.5	5.8	1460	Q4G1M2_EPTBU	Q5hz61 xenopus tro
668	180	5.7	250	Q4G1M2_EPTBU	Q4g1m2 eptatretus
669	180	5.7	369	PGS1_BOVIN	P21809 bos taurus
670	180	5.7	522	LRTM1_PONPY	Q5r6b1 pongo pygma
671	180	5.7	817	Q86P15_DROME	Q86p15 drosophila
672	180	5.7	817	Q9VS84_DROME	Q9vs84 drosophila
673	180	5.7	843	Q7ZTG5_CHICK	Q7ztg5 gallus gall
674	180	5.7	869	Q6E4D6_PETMA	Q4s0c1 tetraodon n
675	179.5	5.7	187	Q61GX3_CAEBR	Q6e4d6 petromyzon
676	179.5	5.7	585	Q5R3F8_HUMAN	Q61gx3 caenorhabdi
677	179.5	5.7	820	LRIG3_MOUSE	Q5r3f8 homo sapien
678	179.5	5.7	1117	Q9ERV0_RAT	Q6p1c6 mus musculu
679	179.5	5.7	4283	Q6E4B8_PETMA	Q9erv0 rattus norv
680	179	5.7	273	Q5M8M9_MOUSE	Q6e4b8 petromyzon
681	179	5.7	314	Q9VT89_DROME	Q5m8m9 mus musculu
682	179	5.7	534	Q9P244_HUMAN	Q9vt89 drosophila
683	179	5.7	700	Q9BJD4_STRPU	Q9p244 homo sapien
684	179	5.7	742	TLR3_MOUSE	Q9bjd4 strongyloce
685	179	5.7	905	Q4LBC9_ONCMY	Q99mb1 mus musculu
686	179	5.7	969	Q5I2M4_SHEEP	Q4lbc9 oncorhynchu
687	179	5.7	1029	Q567L5_BRARE	Q5i2m4 ovis aries
688	178.5	5.7	176		Q567l5 brachydanio

#	Value	Score	Length	N	ID	Organism
689	178.5	5.7	190	2	Q654D8_PETMA	petromyzon
690	178.5	5.7	348	2	Q5RI43_BRARE	brachydanio
691	178.5	5.7	356	1	PGS2_COTJA	coturnix co
692	178.5	5.7	443	2	Q67VV7_ORYSA	oryza sativ
693	178.5	5.7	493	1	AMGO1_HUMAN	homo sapien
694	178.5	5.7	587	2	Q40QJ9_LEIMA	leishmania
695	178.5	5.7	1024	1	POPC_RALSO	ralstonia s
696	178.5	5.7	1063	2	Q5Z666_ORYSA	oryza sativ
697	178.5	5.7	1104	2	Q7XUH4_ORYSA	oryza sativ
698	178.5	5.7	1310	1	GP125_MOUSE	mus musculu
699	178	5.7	187	2	Q6E4H4_PETMA	petromyzon
700	178	5.7	364	2	Q66J59_XENLA	xenopus lae
701	178	5.7	391	2	Q4RQI1_TETNG	tetraodon n
702	178	5.7	488	2	Q4RXQ5_TETNG	tetraodon n
703	178	5.7	522	1	LRTM1_HUMAN	homo sapien
704	178	5.7	894	2	Q9BJD6_STRPU	strongyloce
705	178	5.7	1049	1	TLR7_HUMAN	homo sapien
706	177.5	5.7	1052	2	Q9Y4C4_HUMAN	homo sapien
707	177.5	5.7	1257	2	Q7PNF8_ANOGA	anopheles g
708	177.5	5.7	275	2	Q4G1K5_EPTST	eptatretus
709	177.5	5.7	796	2	Q59HI9_PIG	sus scrofa
710	177.5	5.7	796	2	Q4LDR7_PIG	sus scrofa
711	177.5	5.7	809	2	Q4RMQ1_TETNG	tetraodon n
712	177.5	5.7	1026	2	Q5SMW2_ORYSA	oryza sativ
713	177.5	5.7	1050	1	TLR7_MOUSE	mus musculu
714	177.5	5.7	1050	2	Q548J0_MOUSE	mus musculu
715	177.5	5.7	1360	2	Q7KTA0_DROME	drosophila
716	177.5	5.7	1530	2	Q6D07_HUMAN	homo sapien
717	177.5	5.7	2300	1	CYAA_NEICR	neisseria
718	177.5	5.7	2493	2	Q4P3T1_USTMA	ustilago ma
719	177.5	5.7	2493	2	CYAA_USTMA	ustilago ma
720	177	5.7	187	2	Q6E4H5_PETMA	petromyzon
721	177	5.6	334	2	Q4SBU8_TETNG	tetraodon n
722	177	5.6	343	1	LUM_COTJA	coturnix co
723	177	5.6	347	2	Q58A48_BRARE	brachydanio
724	177	5.6	662	2	Q5RF01_PONPY	pongo pygma
725	177	5.6	666	2	Q702W6_ANOGA	anopheles g
726	177	5.6	670	2	Q5FW85_MOUSE	mus musculu
727	177	5.6	1370	2	Q58NA4_APIME	apis mellif
728	176.5	5.6	187	2	Q6E4M0_PETMA	petromyzon
729	176.5	5.6	520	2	Q5VR46_ORYSA	oryza sativ
730	176.5	5.6	522	1	AMGO2_HUMAN	homo sapien
731	176.5	5.6	522	2	Q4VBP6_HUMAN	homo sapien
732	176.5	5.6	628	2	Q7PVZ6_ANOGA	anopheles g
733	176.5	5.6	856	2	Q59HI7_PIG	sus scrofa
734	176.5	5.6	901	2	Q4SBD4_TETNG	tetraodon n
735	176	5.6	1495	2	LRRC7_RAT	rattus norv
736	176	5.6	1756	2	Q6AWK8_DROME	drosophila
737	176	5.6	249	2	Q4SUM4_TETNG	tetraodon n
738	176	5.6	503	2	Q8LJ87_ORYSA	oryza sativ
739	176	5.6	623	2	Q95S21_DROME	drosophila
740	176	5.6	862	2	Q5GR02_CHICK	gallus gall
741	176	5.6	904	2	Q5TJ59_BOVIN	bos taurus
742	176	5.6	905	2	Q5TJ58_BOVIN	bos taurus
743	176	5.6	906	2	Q4SRZ0_TETNG	tetraodon n
744	176	5.6	1032	2	Q5I2M8_CANFA	canis famil
745	176	5.6	1257	2	Q9VK28_DROME	drosophila
746	176	5.6	1412	1	LAP2_HUMAN	homo sapien
747	175.5	5.6	272	2	Q4KP14_9PETR	ichthyomyzo
748	175.5	5.6	384	2	Q4T0V4_TETNG	tetraodon n
749	175.5	5.6	440	2	Q7TNM3_RAT	rattus norv
750	175.5	5.6	492	1	AMGO1_MOUSE	mus musculu
751	175.5	5.6	1017	1	Q5H718_FUGRU	fugu rubrip
752	175.5	5.6	1490	1	LRRC7_MOUSE	mus musculu
753	175.5	5.6	1731	2	Q4S0D3_TETNG	tetraodon n
754	175	5.6	252	2	Q4G1J2_EPTST	eptatretus
755	175	5.6	343	1	LUM_CHICK	gallus gall
756	175	5.6	429	2	Q8BJ09_MOUSE	mus musculu
757	175	5.6	510	2	Q9BGY6_MACFA	macaca fasc
758	175	5.6	941	2	Q5H722_FUGRU	fugu rubrip
759	175	5.6	973	2	Q6KCC7_ONCMY	oncorhynchu
760	175	5.6	1137	2	Q7QHH1_ANOGA	anopheles g
761	174.5	5.6	190	2	Q6E4E5_PETMA	petromyzon

#	Value	Score	Length	N	ID	Organism
762	174.5	5.6	440	2	Q4J5V4_AZOVI	azotobacter
763	174.5	5.6	512	2	Q9CQ76_MOUSE	m mus muscu
764	174.5	5.6	567	2	Q4SL10_TETNG	tetraodon n
765	174.5	5.6	602	2	Q9CRC8_MOUSE	mus musculu
766	174.5	5.6	602	2	Q8BS83_MOUSE	mus musculu
767	174.5	5.6	602	2	Q78WQ9_MOUSE	mus musculu
768	174.5	5.6	605	2	Q6GPJ5_XENLA	xenopus lae
769	174.5	5.6	795	1	TLR6_MOUSE	mus musculu
770	174.5	5.6	1020	2	Q5ZED4_ORYSA	oryza sativ
771	174.5	5.6	1060	2	Q6ZGM3_ORYSA	oryza sativ
772	174	5.6	490	2	Q4RYL5_TETNG	tetraodon n
773	174	5.6	535	2	Q8RX50_BRANI	brassica ni
774	174	5.6	544	2	Q7Q2W5_ANOGA	anopheles g
775	174	5.6	651	2	Q4QQ2_XENLA	xenopus lae
776	174	5.6	859	1	TLR5_MOUSE	mus musculu
777	174	5.6	951	1	LGR4_RAT	rattus norv
778	173.5	5.5	261	1	Q5M8T1_HUMAN	homo sapien
779	173.5	5.5	337	2	Q4RJX0_TETNG	tetraodon n
780	173.5	5.5	353	2	Q640B1_XENTR	xenopus tro
781	173.5	5.5	364	2	Q6GNX8_XENLA	xenopus lae
782	173.5	5.5	421	1	OMD_HUMAN	homo sapien
783	173.5	5.5	421	2	Q5TBF4_HUMAN	homo sapien
784	173.5	5.5	440	2	Q7TQ25_RAT	rattus norv
785	173.5	5.5	537	1	LGI4_MOUSE	mus musculu
786	173.5	5.5	727	2	Q6GV21_BOVIN	bos taurus
787	173.5	5.5	806	2	Q7TPC5_MOUSE	mus musculu
788	173.5	5.5	826	1	TLR4_PAPAN	papio anubi
789	173.5	5.5	884	2	Q5H720_FUGRU	fugu rubrip
790	173	5.5	252	2	Q4G1I4_EPTST	eptatretus
791	173	5.5	269	2	Q6E4C2_PETMA	petromyzon
792	173	5.5	360	1	PGS2_HORSE	equus cabal
793	173	5.5	470	2	Q9V354_DROME	drosophila
794	173	5.5	539	2	Q503F6_BRARE	brachydanio
795	173	5.5	664	2	Q5UT54_SALSA	salmo salar
796	173	5.5	853	2	Q8CB40_MOUSE	mus musculu
797	173	5.5	925	1	GLHR_ANTEL	anthopleura
798	173	5.5	1459	2	Q7Q0C5_ANOGA	anopheles g
799	173	5.5	1459	2	Q8WRE4_ANOGA	anopheles g
800	172.5	5.5	163	2	Q6E4E2_PETMA	petromyzon
801	172.5	5.5	353	1	KERA_CHICK	gallus gall
802	172.5	5.5	353	1	KERA_COTJA	coturnix co
803	172.5	5.5	359	1	PGS2_HUMAN	homo sapien
804	172.5	5.5	359	1	PGS2_PANTR	pan troglod
805	172.5	5.5	359	2	Q6FH10_HUMAN	homo sapien
806	172.5	5.5	378	2	Q5R294_DROSI	drosophila
807	172.5	5.5	739	2	Q60NV9_CAEBR	caenorhabdi
808	172.5	5.5	823	2	Q8CCW8_MOUSE	mus musculu
809	172.5	5.5	823	2	Q68FM6_MOUSE	mus musculu
810	172.5	5.5	1711	2	Q59DT7_DROME	drosophila
811	172.5	5.5	1850	2	Q59DT8_DROME	drosophila
812	172.5	5.5	1851	2	LAP4_DROME	drosophila
813	172.5	5.5	4256	2	Q8MJF3_CANFA	canis famil
814	172	5.5	339	2	Q4SU68_TETNG	tetraodon n
815	172	5.5	347	2	Q2UT1_BRARE	brachydanio
816	172	5.5	411	2	Q4S9P3_TETNG	tetraodon n
817	172	5.5	577	2	Q8N3K5_HUMAN	homo sapien
818	172	5.5	1134	2	Q65S10_ARATH	arabidopsis
819	172	5.5	1693	2	Q4INH4_GIBZE	gibberella
820	171.5	5.5	378	2	Q5V900_DROME	drosophila
821	171.5	5.5	605	2	Q5M8G4_XENTR	xenopus tro
822	171.5	5.5	683	1	LRCH4_HUMAN	homo sapien
823	171.5	5.5	858	1	TLR5_HUMAN	homo sapien
824	171.5	5.5	858	2	Q5U308_RAT	rattus norv
825	171.5	5.5	859	1	LRRC5_MOUSE	mus musculu
826	171.5	5.5	1589	2	Q9UUQ9_METAN	metarhizium
827	171	5.5	360	1	PGS2_PIG	sus scrofa
828	171	5.5	360	2	Q6DVI1_GECJA	gecko japon
829	171	5.5	552	2	Q8V606_HUMAN	homo sapien
830	171	5.5	643	2	Q502J4_BRARE	brachydanio
831	171	5.5	833	1	TLR4_FELCA	felis silve
832	171	5.5	1317	2	Q5TUS9_ANOGA	anopheles g
833	170.5	5.4	246	2	Q6E4J1_PETMA	petromyzon
834	170.5	5.4	359	2	Q4RSD2_MACFA	macaca fasc

No.	Score	Prob	Len	ID	n	Accession	Organism
835	170.5	5.4	373	ASPN_MOUSE	1	Q99mq4	mus musculu
836	170.5	5.4	741	Q8KTF7_LISMO	2	Q8ktf7	listeria mo
837	170.5	5.4	1031	Q512M7_FELCA	2	Q512m7	felis silve
838	170.5	5.4	1031	Q8HZ52_FELCA	2	Q8hz52	felis silve
839	170.5	5.4	2145	CYAA_PODAN	1	Q01513	podospora a
840	170	5.4	187	Q6E4D9_PETMA	2	Q6e4d9	petromyzon
841	170	5.4	364	LRC19_MOUSE	1	Q8bzt5	mus musculu
842	170	5.4	572	Q4QGJ6_LEIMA	2	Q4qgj6	leishmania
843	170	5.4	883	Q4VAM0_HUMAN	2	Q4vam0	homo sapien
844	170	5.4	907	LGR5_HUMAN	1	O75473	homo sapien
845	170	5.4	907	Q4VAM2_HUMAN	2	Q4vam2	homo sapien
846	170	5.4	1024	Q84IE6_RALSO	2	Q84ie6	ralstonia s
847	170	5.4	1032	Q59ER8_HUMAN	1	Q59er8	homo sapien
848	170	5.4	1471	Q7KW92_DROME	2	Q7kw92	drosophila
849	169.5	5.4	352	KERA_BOVIN	2	O62702	bos taurus
850	169.5	5.4	366	Q8BX06_MOUSE	2	Q8bx06	m mus muscu
851	169.5	5.4	493	AMGO1_RAT	1	O82zd7	rattus norv
852	169.5	5.4	651	Q4T8T9_TETNG	2	Q4t8t9	tetraodon n
853	169.5	5.4	760	Q9TOK5_ARATH	2	Q9tok5	arabidopsis
854	169.5	5.4	876	Q67WE5_ORYSA	2	Q67we5	oryza sativ
855	169.5	5.4	991	Q6RSN8_MOUSE	2	Q6rsn8	mus musculu
856	169.5	5.4	1271	FLII_MOUSE	1	Q9jj28	mus musculu
857	169	5.4	217	Q66WJ6_FELCA	1	Q66wj6	felis silve
858	169	5.4	273	Q5XPY6_ICTPU	2	Q5xpy6	ictalurus p
859	169	5.4	279	Q58HK2_TRASC	2	Q58hk2	trachemys s
860	169	5.4	354	PGS2_MOUSE	1	P28654	mus musculu
861	169	5.4	360	Q6JOY6_PAROL	2	Q6joy6	paralichthy
862	169	5.4	757	Q69MS7_ORYSA	2	Q69ms7	oryza sativ
863	169	5.4	839	Q9RX57_DEIRA	2	Q9rx57	deinococcus
864	169	5.4	1175	Q4RER3_TETNG	2	Q4rer3	tetraodon n
865	169	5.4	1288	Q624K5_CAEBR	2	Q624k5	caenorhabdi
866	169	5.4	1658	Q4PLE9_FUSPR	1	Q4ple9	fusarium pr
867	168.5	5.4	246	Q4KP10_LAMAP	2	Q4kp10	lampetra ap
868	168.5	5.4	255	Q66WJ3_FELCA	2	Q66wj3	felis silve
869	168.5	5.4	333	Q4SY28_TETNG	2	Q4sy28	tetraodon n
870	168.5	5.4	343	Q50IS3_BRARE	2	Q50is3	brachydanio
871	168.5	5.4	353	Q7SYS8_XENLA	2	Q7sys8	xenopus lae
872	168.5	5.4	363	Q8C8A7_MOUSE	1	Q8c8a7	mus musculu
873	168.5	5.4	378	Q5R264_DROSE	2	Q5r264	drosophila
874	168.5	5.4	619	Q6K8KO_ORYSA	2	Q6k8ko	oryza sativ
875	168.5	5.4	685	Q6T545_LISMO	2	Q6t545	listeria mo
876	168.5	5.4	694	Q61P91_CAEBR	2	Q61p91	caenorhabdi
877	168.5	5.4	728	Q6T546_LISMO	2	Q6t546	listeria mo
878	168.5	5.4	744	Q8KTF6_LISMO	2	Q8ktf6	listeria mo
879	168.5	5.4	907	LGR5_MOUSE	2		mus musculu
880	168.5	5.4	1036	Q9FN37_ARATH	1	Q9fn37	arabidopsis
881	168.5	5.4	1360	Q9NDI1_DROME	1	Q9ndi1	drosophila
882	168.5	5.4	1724	Q4H4B6_BRARE	2	Q4h4b6	brachydanio
883	168	5.4	351	Q65YW8_XENLA	2	Q65yw8	xenopus lae
884	168	5.4	402	Q72U35_LEPIC	2	Q72u35	leptospira
885	168	5.4	753	Q9NRE6_HUMAN	2	Q9nre6	homo sapien
886	168	5.4	773	Q5NE35_LISMO	1	Q5ne35	listeria mo
887	168	5.4	951	LGR4_HUMAN	2		homo sapien
888	168	5.4	977	Q7XS37_ORYSA	2	Q7xs37	oryza sativ
889	167.5	5.4	147	Q8GVW0_PIG	1	Q8gvw0	sus scrofa
890	167.5	5.4	351	Q9TT00_PIG	1	Q9tt00	sus scrofa
891	167.5	5.4	360	KERA_MOUSE	2	O35367	mus musculu
892	167.5	5.4	378	PGS2_SHEEP	2		ovis aries
893	167.5	5.4	396	Q72U36_LEPIC	1	Q72u36	leptospira
894	167.5	5.4	422	Q8C3D9_MOUSE	2	Q8c3d9	mus musculu
895	167.5	5.4	694	OMD_BOVIN	2	O77742	bos taurus
896	167.5	5.4	917	Q4RYL2_TETNG	1	Q4ryl2	tetraodon n
897	167.5	5.4	1174	Q75GM9_ORYSA	2	Q75gm9	oryza sativ
898	167	5.3	537	Q6P2A4_RAT	1	Q6p2a4	rattus norv
899	167	5.3	582	Q6AYI5_RAT	2	Q6ayi5	rattus norv
900	167	5.3	633	Q8F3F6_LEPIN	2	Q8f3f6	leptospira
901	167	5.3	743	Q84CF7_LISMO	1	Q84cf7	listeria mo
902	167	5.3	744	Q8KTF4_LISMO	2	Q8ktf4	listeria mo
903	167	5.3	794	Q6YW99_ORYSA	2	Q6yw99	oryza sativ
904	167	5.3	838	Q9WV82_CRIGR	2	Q9wv82	cricetulus
905	167	5.3	939	Q4SZU0_TETNG	1	Q4szu0	tetraodon n
906	167	5.3	1112	Q41397_LYCPM	2	Q41397	lycopersico
907	167	5.3	1112	Q41398_LYCPM	2	Q41398	lycopersico
908	167	5.3	1112	Q4G2W2_LYCPM	2	Q4g2w2	lycopersico
909	167	5.3	1263	Q4SID1_TETNG	2	Q4sid1	tetraodon n
910	167	5.3	1845	Q5QNQ9_MOUSE	2	Q5qnq9	mus musculu
911	166.5	5.3	163	Q6E4D4_PETMA	2	Q6e4d4	petromyzon
912	166.5	5.3	483	Q5NE36_LISMO	2	Q5ne36	listeria mo
913	166.5	5.3	549	Q9SVW8_ARATH	2	Q9svw8	arabidopsis
914	166.5	5.3	582	Q5R423_PONPY	2	Q5r423	pongo pygma
915	166.5	5.3	739	Q84CF6_LISMO	2	Q84cf6	listeria mo
916	166.5	5.3	741	Q8KTF0_LISMO	2	Q8ktf0	listeria mo
917	166.5	5.3	741	Q8KTF9_LISMO	2	Q8ktf9	listeria mo
918	166.5	5.3	743	Q95RV9_DROME	2	Q95rv9	drosophila
919	166.5	5.3	743	Q8KTF2_LISMO	2	Q8ktf2	listeria mo
920	166.5	5.3	744	Q8KHN1_LISMO	2	Q8khn1	listeria mo
921	166.5	5.3	744	Q8KI88_LISMO	2	Q8ki88	listeria mo
922	166.5	5.3	744	Q8KTF1_LISMO	2	Q8ktf1	listeria mo
923	166.5	5.3	744	Q8KTF5_LISMO	2	Q8ktf5	listeria mo
924	166.5	5.3	744	Q8KTF8_LISMO	2	Q8ktf8	listeria mo
925	166.5	5.3	746	Q8KTF3_LISMO	2	Q8ktf3	listeria mo
926	166.5	5.3	792	Q5NE37_LISMO	2	Q5ne37	listeria mo
927	166.5	5.3	800	INLA_LISMF	1	Q723k6	listeria mo
928	166.5	5.3	800	INLA_LISMO	1	P25146	listeria mo
929	166.5	5.3	1012	Q95YI6_ASTPE	2	Q95yi6	asterina pe
930	166.5	5.3	1115	Q652D9_ORYSA	2	Q652d9	oryza sativ
931	166.5	5.3	1215	Q60PY2_CAEBR	2	Q60py2	caenorhabdi
932	166.5	5.3	1270	Q7QHP7_ANOGA	2	Q7qhp7	anopheles g
933	166.5	5.3	1280	Q95YI7_ASTPE	2	Q95yi7	asterina pe
934	166.5	5.3	3204	Q6X248_9ALPH	2	Q6x248	bovine herp
935	166	5.3	163	Q6E4F8_PETMA	2	Q6e4f8	petromyzon
936	166	5.3	245	Q4KP01_LAMAP	2	Q4kp01	lampetra ap
937	166	5.3	426	Q72TC3_LEPIC	2	Q72tc3	leptospira
938	166	5.3	768	Q4SSE3_TETNG	2	Q4sse3	tetraodon n
939	166	5.3	806	Q6P690_RAT	1	Q6p690	rattus norv
940	166	5.3	835	TLR4_RAT	2	Q9qx05	rattus norv
941	166	5.3	1030	Q512M3_PIG	2	Q512m3	sus scrofa
942	166	5.3	1030	Q865R8_PIG	2	Q865r8	sus scrofa
943	166	5.3	1110	Q7G768_ORYSA	2	Q7g768	oryza sativ
944	166	5.3	1110	Q94LN2_ORYSA	2	Q94ln2	oryza sativ
945	166	5.3	1221	Q9NSZ3_CAEEL	2	Q9nsz3	caenorhabdi
946	166	5.3	2139	Q4PDW0_USTMA	2	Q4pdw0	ustilago ma
947	165.5	5.3	327	Q5RHE5_BRARE	2	Q5rhe5	brachydanio
948	165.5	5.3	360	PGS2_BOVIN	1	P21793	bos taurus
949	165.5	5.3	360	PGS2_CANFA	2	Q29393	canis famil
950	165.5	5.3	526	Q7XJS3_ARATH	2	Q7xjs3	arabidopsis
951	165.5	5.3	641	Q5H716_FUGRU	2	Q5h716	fugu rubrip
952	165.5	5.3	1101	Q59H95_HUMAN	2	Q59h95	homo sapien
953	165.5	5.3	1256	FLII_DROME	1	Q24020	drosophila
954	165.5	5.3	1269	FLII_HUMAN	1	Q13045	homo sapien
955	165.5	5.3	1269	Q5R4G9_PONPY	2	Q5r4g9	pongo pygma
956	165	5.3	283	Q4RX02_TETNG	2	Q4rx02	tetraodon n
957	165	5.3	436	Q5R6F8_PONPY	2	Q5r6f8	pongo pygma
958	165	5.3	902	Q7RYP2_NEUCR	2	Q7ryp2	neurospora
959	165	5.3	994	Q9C637_ARATH	2	Q9c637	arabidopsis
960	165	5.3	1135	Q7XS12_ORYSA	2	Q7xs12	oryza sativ
961	165	5.3	1154	Q7GHH4_ANOGA	2	Q7ghh4	anopheles g
962	164.5	5.2	235	Q4G1H9_EPTST	2	Q4g1h9	eptatretus
963	164.5	5.2	468	Q4LVE2_9BURK	2	Q4lve2	burkholderi
964	164.5	5.2	582	SHOC2_HUMAN	1	Q9uq13	homo sapien
965	164.5	5.2	582	Q5VZS9_HUMAN	2	Q5vzs9	homo sapien
966	164.5	5.2	582	Q5RAV5_PONPY	2	Q5rav5	pongo pygma
967	164.5	5.2	734	Q5R7N1_PONPY	2	Q5r7n1	pongo pygma
968	164.5	5.2	805	Q658W7_HUMAN	2	Q658w7	homo sapien
969	164.5	5.2	819	Q659A9_HUMAN	2	Q659a9	homo sapien
970	164.5	5.2	858	LRRC5_HUMAN	1	Q711w4	homo sapien
971	164	5.2	257	LRRC3_MOUSE	1	P59034	mus musculu
972	164	5.2	257	Q543Z4_MOUSE	2	Q543z4	mus musculu
973	164	5.2	426	Q8F213_LEPIN	2	Q8f213	leptospira
974	164	5.2	515	Q60MT7_CAEBR	2	Q60mt7	caenorhabdi
975	164	5.2	559	Q6OUG7_CAEBR	2	Q6oug7	caenorhabdi
976	164	5.2	570	Q8L3T8_ORYSA	2	Q8l3t8	oryza sativ
977	164	5.2	611	Q7TQ62_MOUSE	2	Q7cq62	mus musculu
978	164	5.2	696	SLIK1_HUMAN	1	Q60px8	homo sapien
979	164	5.2	696	SLIK1_MOUSE	1	Q810c1	mus musculu
980	164	5.2	696	Q5USI6_HUMAN	2	Q5usi6	homo sapien

Left column (entries 981–1053)

Accession	Species	ID	Cnt	Length	Exp	Bits	No.
Q5rac4	pongo pygma	Q5RAC4_PONPY	2	696	5.2	164	981
Q69z70	mus musculu	Q69Z70_MOUSE	2	760	5.2	164	982
Q7qff0	anopheles g	Q7QFF0_ANOGA	2	805	5.2	164	983
Q9hbx8	homo sapien	LGR6_HUMAN	1	828	5.2	164	984
Q7q8i8	anopheles g	Q7Q8I8_ANOGA	2	833	5.2	164	985
Q8miq2	oryctolagus	Q8MIQ2_RABIT	2	839	5.2	164	986
Q6pcd4	homo sapien	Q6PCD4_HUMAN	2	870	5.2	164	987
O15455	homo sapien	TLR3_HUMAN	1	904	5.2	164	988
Q504w0	homo sapien	Q504W0_HUMAN	2	904	5.2	164	989
Q4val2	homo sapien	Q4VAL2_HUMAN	2	904	5.2	164	990
Q865b9	canis famil	Q865B9_CANFA	2	1032	5.2	164	991
Q7sc01	neurospora	Q7SC01_NEUCR	2	1395	5.2	164	992
Q5sva2	homo sapien	Q5SVA2_HUMAN	2	1913	5.2	164	993
O00468	homo sapien	AGRN_HUMAN	1	2045	5.2	164	994
Q60fe1	homo sapien	Q60FE1_HUMAN	2	163	5.2	163.5	995
Q6e4e0	petromyzon	Q6E4E0_PETMA	2	166	5.2	163.5	996
Q6e4i0	petromyzon	Q6E4IO_PETMA	2	180	5.2	163.5	997
Q6e4h7	petromyzon	Q6E4H7_PETMA	2	362	5.2	163.5	998
Q5o2f2	brachydanio	Q5O2F2_BRARE	2	370	5.2	163.5	999
Q9de04	oreochromis	Q9DE04_ORENI	2	582	5.2	163.5	1000
Q5r5r1	pongo pygma	Q5R5R1_PONPY	2	671	5.2	163.5	1001
Q53gz4	homo sapien	Q53GZ4_HUMAN	2	786	5.2	163.5	1002
O48809	arabidopsis	O48809_ARATH	2	359	5.2	163	1003
Q9de03	oreochromis	Q9DE03_ORENI	2	452	5.2	163	1004
Q4rqb6	tetraodon n	Q4RQB6_TETNG	2	501	5.2	163	1005
Q6zh85	oryza sativ	Q6ZH85_ORYSA	2	524	5.2	163	1006
Q8r378	mus musculu	Q8R378_MOUSE	2	582	5.2	163	1007
O88520	mus musculu	SHOC2_MOUSE	1	929	5.2	163	1008
Q6p9n3	mus musculu	Q6P9N3_MOUSE	2	933	5.2	163	1009
Q9bjd5	strongyloce	Q9BJD5_STRPU	2	961	5.2	163	1010
Q76ct7	paralichthy	Q76CT7_PAROL	2	961	5.2	163	1011
Q9biw9	caenorhabdi	Q9BIW9_CAEEL	2	1221	5.2	163	1012
Q80u72	mus musculu	LAP4_MOUSE	1	1612	5.2	163	1013
Q9v428	drosophila	Q9V428_DROME	2	283	5.2	162.5	1014
Q5xih1	rattus norv	Q5XIH1_RAT	2	375	5.2	162.5	1015
Q8f118	leptospira	Q8F118_LEPIN	2	452	5.2	162.5	1016
Q9vek6	drosophila	Q9VEK6_DROME	2	494	5.2	162.5	1017
Q86pb5	drosophila	Q86PB5_DROME	2	527	5.2	162.5	1018
Q8mqm0	drosophila	Q8MQM0_DROME	2	641	5.2	162.5	1019
Q4r6h5	macaca fasc	Q4R6H5_MACFA	2	700	5.2	162.5	1020
Q5h717	fugu rubrip	Q5H717_FUGRU	2	1045	5.2	162.5	1021
Q4g1h3	eptatretus	Q4G1H3_EPTST	2	234	5.2	162	1022
Q9ug10	homo sapien	Q9UG10_HUMAN	2	242	5.2	162	1023
Q7qli8	anopheles g	Q7QLI8_ANOGA	2	375	5.2	162	1024
Q72517	homo sapien	Q72517_HUMAN	2	613	5.2	162	1025
Q6uxl8	homo sapien	Q6UXL8_HUMAN	2	642	5.2	162	1026
Q5vvz2	homo sapien	Q5VVZ2_HUMAN	2	642	5.2	162	1027
Q8c2m4	mus musculu	Q8C2M4_MOUSE	2	649	5.2	162	1028
Q6pir3	homo sapien	Q6PIR3_HUMAN	2	661	5.2	162	1029
Q5vvz3	homo sapien	Q5VVZ3_HUMAN	2	661	5.2	162	1030
Q7qis8	anopheles g	Q7QIS8_ANOGA	2	942	5.2	162	1031
Q628y3	oryza sativ	Q628Y3_ORYSA	2	1040	5.2	162	1032
Q70hk8	anopheles g	Q7OHK8_ANOGA	2	259	5.1	161.5	1033
Q6wcd4	bos taurus	Q6WCD4_BOVIN	2	268	5.1	161.5	1034
Q6wcd5	bos taurus	Q6WCD5_BOVIN	2	351	5.1	161.5	1035
Q8sq55	bos taurus	Q8SQ55_BOVIN	2	507	5.1	161.5	1036
Q4sl20	tetraodon n	Q4SL20_TETNG	2	519	5.1	161.5	1037
Q5rki5	rattus norv	Q5RKI5_RAT	2	841	5.1	161.5	1038
Q7qf88	anopheles g	Q7QF88_ANOGA	2	841	5.1	161.5	1039
Q8mpp6	caenorhabdi	Q8MPP6_CAEEL	2	841	5.1	161.5	1040
O22875	caenorhabdi	O22875_CAEEL	2	1193	5.1	161.5	1041
Q93377	caenorhabdi	Q93377_CAEEL	2	1270	5.1	161.5	1042
				397	5.1	161	1043
				558	5.1	161	1044
				559	5.1	161	1045
				586	5.1	161	1046
					5.1	161	1047
					5.1	161	1048
Q01819	drosophila	CONN_DROME	1	682	5.1	161	1049
Q6awm0	drosophila	Q6AWM0_DROME	2	691	5.1	161	1050
Q9sls3	nicotiana t	Q9SLS3_TOBAC	2	861	5.1	161	1051
Q7tni8	rattus norv	Q7TNI8_RAT	2	905	5.1	161	1052
Q801f9	carassius a	Q801F9_CARAU	2	945	5.1	161	1053

Right column (entries 1054–1126)

No.	Bits	Exp	Length	ID	Cnt	Species	Accession
1054	161	5.1	1019	Q4RW99_TETNG	2	tetraodon n	Q4rw99
1055	160.5	5.1	487	Q7QKY2_ANOGA	2	anopheles g	Q7qky2
1056	160.5	5.1	519	AMGO2_MOUSE	1	mus musculu	Q80zd9
1057	160.5	5.1	519	Q4VBE6_MOUSE	2	mus musculu	Q4vbe6
1058	160.5	5.1	664	Q5EWY7_CTEID	2	ctenopharyn	Q5ewy7
1059	160.5	5.1	1446	Q9VBZ0_DROME	2	drosophila	Q9vbz0
1060	160.5	5.1	2910	O55225_MOUSE	2	mus musculu	O55225
1061	160.5	5.1	3889	Q6SSE8_CHLRE	2	chlamydomon	Q6sse8
1062	160	5.1	258	Q4GLJ6_EPTST	2	eptatretus	Q4glj6
1063	160	5.1	518	Q4R5R9_MACFA	2	macaca fasc	Q4r5r9
1064	160	5.1	744	O65375_ARATH	2	arabidopsis	O65375
1065	160	5.1	950	Q5H723_FUGRU	2	fugu rubrip	Q5h723
1066	160	5.1	1050	Q9BN18_DROME	2	drosophila	Q9bn18
1067	160	5.1	1080	Q69P46_ORYSA	2	oryza sativ	Q69p46
1068	160	5.1	1096	Q8W556_ARATH	2	arabidopsis	Q8w556
1069	160	5.1	1402	LAP2_MOUSE	1	mus musculu	Q80th2
1070	160	5.1	1496	Q92626_HUMAN	2	homo sapien	Q92626
1071	159.5	5.1	187	Q6E4I5_PETMA	2	petromyzon	Q6e4i5
1072	159.5	5.1	235	Q4G1I5_EPTST	2	eptatretus	Q4g1i5
1073	159.5	5.1	412	Q5MIQ1_AEDAL	2	aedes albop	Q5miq1
1074	159.5	5.1	494	Q9LHF1_ARATH	2	arabidopsis	Q9lhf1
1075	159.5	5.1	520	AMGO2_RAT	2	rattus norv	Q7tnj4
1076	159.5	5.1	636	Q8SQH3_CANFA	2	canis famil	Q8sqh3
1077	159.5	5.1	722	Q4KMG2_HUMAN	2	homo sapien	Q4kmg2
1078	159.5	5.1	1112	O64486_ARATH	2	arabidopsis	O64486
1079	159	5.1	257	LRRC3_RAT	2	rattus norv	P59035
1080	159	5.1	524	LRRC1_HUMAN	1	homo sapien	Q9btt6
1081	159	5.1	524	Q5TGN3_HUMAN	2	homo sapien	Q5tgn3
1082	159	5.1	543	Q8S7M7_ORYSA	2	oryza sativ	Q8s7m7
1083	159	5.1	550	LGI2_MOUSE	1	mus musculu	Q8k4z0
1084	159	5.1	626	Q9NDD1_LEITR	2	leishmania	Q9ndd1
1085	159	5.1	671	Q60YZ3_CAEBR	2	caenorhabdi	Q60yz3
1086	159	5.1	695	Q93539_CAEEL	2	caenorhabdi	Q93539
1087	159	5.1	964	Q86U22_HUMAN	2	homo sapien	Q86u22
1088	159	5.1	984	RIN3_HUMAN	1	homo sapien	Q8tb24
1089	159	5.1	985	Q76LB3_HUMAN	2	homo sapien	Q76lb3
1090	159	5.1	1119	Q8ZOH2_ANASP	2	anabaena sp	Q8z0h2
1091	158.5	5.1	163	Q6E4E4_PETMA	2	petromyzon	Q6e4e4
1092	158.5	5.1	166	Q6E4E6_PETMA	2	petromyzon	Q6e4e6
1093	158.5	5.1	242	Q4SSH2_TETNG	2	tetraodon n	Q4ssh2
1094	158.5	5.1	371	Q4TSR8_TETNG	2	tetraodon n	Q4tsr8
1095	158.5	5.1	417	O15828_LEICH	2	leishmania	O15828
1096	158.5	5.1	656	Q19312_CAEEL	2	caenorhabdi	Q19312
1097	158.5	5.1	738	Q93373_CAEEL	2	caenorhabdi	Q93373
1098	158.5	5.1	943	Q4SI33_TETNG	2	tetraodon n	Q4si33
1099	158.5	5.1	953	Q9V701_DROME	2	drosophila	Q9v701
1100	158.5	5.1	1007	Q8MQU9_AEDAE	2	aedes aegyp	Q8mqu9
1101	158.5	5.1	1032	TLR8_MOUSE	2	mus musculu	P58682
1102	158.5	5.1	1061	Q655V6_ORYSA	2	oryza sativ	Q655v6
1103	158.5	5.1	1123	Q6SXS7_ORYSA	2	oryza sativ	Q6sxs7
1104	158.5	5.1	1181	Q7ZZ35_BRARE	2	brachydanio	Q7zz35
1105	158.5	5.1	1202	CSKI2_HUMAN	1	homo sapien	Q8wxe0
1106	158.5	5.1	1300	Q9NKD6_DROME	2	drosophila	Q9nkd6
1107	158	5.0	239	Q4KP19_9PETR	2	ichthyomyzo	Q4kp19
1108	158	5.0	249	Q4KP07_LAMAP	2	lampetra ap	Q4kp07
1109	158	5.0	317	Q96B32_HUMAN	2	homo sapien	Q96b32
1110	158	5.0	352	KERA_HUMAN	1	homo sapien	O60938
1111	158	5.0	377	Q72U33_LEPIC	2	leptospira	Q72u33
1112	158	5.0	510	Q9NIR8_DICDI	2	dictyosteli	Q9nir8
1113	158	5.0	531	Q5TW51_ANOGA	2	anopheles g	Q5tw51
1114	158	5.0	677	Q5XPY7_ICTPU	2	ictalurus p	Q5xpy7
1115	158	5.0	741	Q9VJA9_DROME	2	drosophila	Q9vja9
1116	158	5.0	838	Q4SWS3_TETNG	2	tetraodon n	Q4sws3
1117	158	5.0	879	Q68CI3_ONCMY	2	oncorhynchu	Q68ci3
1118	158	5.0	909	Q6ZRC2_HUMAN	2	homo sapien	Q6zrc2
1119	158	5.0	1032	Q56R09_AOTNA	2	aotus nancy	Q56r09
1120	158	5.0	5703	MUC5B_HUMAN	1	homo sapien	Q9hc84
1121	157.5	5.0	163	Q6E4I4_PETMA	2	petromyzon	Q6e4i4
1122	157.5	5.0	224	Q9DE01_BRARE	2	brachydanio	Q9de01
1123	157.5	5.0	272	Q7KWF0_DROME	2	drosophila	Q7kwf0
1124	157.5	5.0	276	Q7PSP4_ANOGA	2	anopheles g	Q7psp4
1125	157.5	5.0	396	Q5DZ80_VIBF1	2	vibrio fisc	Q5dz80
1126	157.5	5.0	655	Q4RW74_TETNG	2	tetraodon n	Q4rw74

Index	Score	Val	Length	Ct	ID	Accession	Organism
1127	157.5	5.0	861	2	Q50TQ5_ENTHI	Q50tq5	entamoeba h
1128	157.5	5.0	1102	2	Q4RZY0_TETNG	Q4rzy0	tetraodon n
1129	157.5	5.0	2657	2	Q4S189_TETNG	Q4s189	tetraodon n
1130	157	5.0	266	2	Q7Q1P7_ANOGA	Q7q1p7	anopheles g
1131	157	5.0	273	2	Q9NUU4_HUMAN	Q9nuu4	homo sapien
1132	157	5.0	377	2	Q8F119_LEPIN	Q8f119	leptospira
1133	157	5.0	444	2	Q9H5H8_HUMAN	Q9h5h8	homo sapien
1134	157	5.0	592	2	Q7L236_HUMAN	Q7l236	homo sapien
1135	157	5.0	613	2	Q940E8_MAIZE	Q940e8	zea mays (m
1136	157	5.0	622	2	Q8N3B0_HUMAN	Q8n3b0	homo sapien
1137	157	5.0	680	1	LRCH4_MOUSE		mus musculu
1138	157	5.0	796	2	Q6NSJ5_HUMAN	Q6nsj5	homo sapien
1139	157	5.0	903	2	Q6IWL5_BRARE	Q6iwl5	brachydanio
1140	157	5.0	1032	2	Q5I2M6_RAT	Q5i2m6	rattus norv
1141	157	5.0	1032	2	Q6YIS0_RAT	Q6yis0	rattus norv
1142	156.5	5.0	305	2	Q50Q05_ENTHI	Q50q05	entamoeba h
1143	156.5	5.0	360	1	PGS2_RABIT		oryctolagus
1144	156.5	5.0	376	1	FMOD_HUMAN		homo sapien
1145	156.5	5.0	428	2	Q9VDD4_DROME	Q9vdd4	drosophila
1146	156.5	5.0	487	2	Q7Q087_ANOGA	Q7q087	anopheles g
1147	156.5	5.0	505	2	Q4RVS9_TETNG	Q4rvs9	tetraodon n
1148	156.5	5.0	524	2	Q6AXP5_RAT	Q6axp5	rattus norv
1149	156.5	5.0	551	2	Q5ZB68_ORYSA	Q5zb68	oryza sativ
1150	156.5	5.0	711	2	Q9SPM1_LYCES	Q9spm1	lycopersico
1151	156.5	5.0	887	1	UFO_HUMAN		homo sapien
1152	156.5	5.0	980	2	Q92UI0_ARATH	Q92ui0	arabidopsis
1153	156.5	5.0	1179	2	Q7PWD3_ANOGA	Q7pwd3	anopheles g
1154	156.5	5.0	1301	2	Q9VZ81_DROME	Q9vz81	drosophila
1155	156.5	5.0	1766	2	Q6XHA8_DICDI	Q6xha8	dictyosteli
1156	156.5	5.0	1867	2	Q54M77_DICDI	Q54m77	dictyosteli
1157	156	5.0	163	2	Q6E4D2_PETMA	Q6e4d2	petromyzon
1158	156	5.0	163	2	Q6E4F5_PETMA	Q6e4f5	petromyzon
1159	156	5.0	257	1	LRRC3_HUMAN		homo sapien
1160	156	5.0	354	1	PGS2_RAT		rattus norv
1161	156	5.0	422	2	Q4RH13_TETNG	Q4rh13	tetraodon n
1162	156	5.0	469	2	Q9W128_DROME	Q9w128	drosophila
1163	156	5.0	547	2	Q4QGI6_LEIMA	Q4qgi6	leishmania
1164	156	5.0	552	2	Q8K375_MOUSE	Q8k375	mus musculu
1165	156	5.0	575	2	Q571F2_MOUSE	Q571f2	mus musculu
1166	156	5.0	594	2	Q9U3A0_CAEEL	Q9u3a0	caenorhabdi
1167	156	5.0	643	2	Q6QI48_RAT	Q6qi48	rattus norv
1168	156	5.0	704	2	Q4QGK1_LEIMA	Q4qgk1	leishmania
1169	156	5.0	940	2	Q8T753_BRAFL	Q8t753	branchiosto
1170	156	5.0	953	2	Q6I7Q9_CAEBR	Q6i7q9	caenorhabdi
1171	156	5.0	1039	1	Q86BL1_DROME	Q86bl1	drosophila
1172	155.5	5.0	332	2	Q6C2U8_YARLI	Q6c2u8	yarrowia li
1173	155.5	5.0	338	2	Q6YEX8_CHICK	Q6yex8	gallus gall
1174	155.5	5.0	367	2	Q8BK43_MOUSE	Q8bk43	mus musculu
1175	155.5	5.0	664	2	Q5EWY6_CTEID	Q5ewy6	ctenopharyn
1176	155.5	5.0	980	2	Q80WA0_MOUSE	Q80wa0	mus musculu
1177	155.5	5.0	1102	2	Q8KC98_CHLTE	Q8kc98	chlorobium
1178	155.5	5.0	1135	2	Q84RP6_ARATH	Q84rp6	arabidopsis
1179	155.5	5.0	1285	2	CRUM2_HUMAN		homo sapien
1180	155.5	5.0	1334	2	Q9RKR5_STRCO	Q9rkr5	streptomyce
1181	155.5	4.9	347	2	Q9DE00_PETMA	Q9de00	petromyzon
1182	155	4.9	504	1	AMGO3_HUMAN		homo sapien
1183	155	4.9	576	2	Q6Z8P4_ORYSA	Q6z8p4	oryza sativ
1184	155	4.9	719	2	Q8VJQ6_MYCTU	Q8vjq6	mycobacteri
1185	155	4.9	825	2	Q62JU8_BURMA	Q62ju8	burkholderi
1186	155	4.9	961	2	P90920_CAEEL	P90920	caenorhabdi
1187	155	4.9	1041	1	TLR8_HUMAN		homo sapien
1188	154.5	4.9	219	2	Q90WZ2_CHICK	Q90wz2	gallus gall
1189	154.5	4.9	246	2	Q4KP18_9PETR	Q4kp18	ichthyomyzo
1190	154.5	4.9	376	2	Q8IV47_HUMAN	Q8iv47	homo sapien
1191	154.5	4.9	524	1	LRRC1_MOUSE		mus musculu
1192	154.5	4.9	548	2	Q9VJU1_DROME	Q9vju1	drosophila
1193	154.5	4.9	606	2	Q571M3_MOUSE	Q571m3	mus musculu
1194	154.5	4.9	631	2	Q8TNI4_METAC	Q8tni4	methanosarc
1195	154.5	4.9	1013	2	Q9M0G7_ARATH	Q9m0g7	arabidopsis
1196	154.5	4.9	1109	2	Q6YT77_ORYSA	Q6yt77	oryza sativ
1197	154.5	4.9	1143	2	Q9SUB9_ARATH	Q9sub9	arabidopsis
1198	154.5	4.9	1192	1	EXS_ARATH		arabidopsis
1199	154.5	4.9	1961	2	Q6MG89_RAT	Q6mg89	rattus norv
1200	154.5	4.9	2461	2	Q5SD06_HUMAN	Q5sd06	homo sapien
1201	154.5	4.9	2517	1	NCOR2_HUMAN	Q9y618	h nuclear r
1202	154	4.9	399	2	Q8STX6_ENCCU	Q8stx6	encephalito
1203	154	4.9	458	2	Q9VU13_DROME	Q9vu13	drosophila
1204	154	4.9	491	2	Q6KAP0_MOUSE	Q6kap0	mus musculu
1205	154	4.9	530	2	P97830_RAT	P97830	rattus norv
1206	154	4.9	584	2	O49751_ARATH	O49751	arabidopsis
1207	154	4.9	584	2	Q8L7Z2_ARATH	Q8l7z2	arabidopsis
1208	154	4.9	812	2	Q9VFY9_DROME	Q9vfy9	drosophila
1209	154	4.9	825	2	Q63UU8_BURPS	Q63uu8	burkholderi
1210	154	4.9	953	2	Q8VYG7_ARATH	Q8vyg7	arabidopsis
1211	154	4.9	965	2	Q5H724_FUGRU	Q5h724	fugu rubrip
1212	154	4.9	1845	2	Q8OUA8_MOUSE	Q8oua8	mus musculu
1213	153.5	4.9	163	2	Q6E4L8_PETMA	Q6e4l8	petromyzon
1214	153.5	4.9	166	2	Q6E4G9_PETMA	Q6e4g9	petromyzon
1215	153.5	4.9	246	2	Q4KP02_LAMAP	Q4kp02	lampetra ap
1216	153.5	4.9	366	2	Q5R858_PONPY	Q5r858	pongo pygma
1217	153.5	4.9	389	2	Q4RHN9_TETNG	Q4rhn9	tetraodon n
1218	153.5	4.9	403	2	Q96CX6_HUMAN	Q96cx6	homo sapien
1219	153.5	4.9	526	2	Q5BL36_BRARE	Q5bl36	brachydanio
1220	153.5	4.9	655	2	Q9FBR7_STRCO	Q9fbr7	streptomyce
1221	153.5	4.9	685	2	Q72TH0_LEPIC	Q72th0	leptospira
1222	153.5	4.9	685	2	Q8FIV0_LEPIN	Q8fiv0	leptospira
1223	153.5	4.9	802	2	Q8L4U4_ORYSA	Q8l4u4	oryza sativ
1224	153.5	4.9	864	2	Q8LPG4_ARATH	Q8lpg4	arabidopsis
1225	153.5	4.9	864	2	Q9T033_ARATH	Q9t033	arabidopsis
1226	153.5	4.9	894	2	Q8NSL2_HUMAN	Q8nsl2	homo sapien
1227	153.5	4.9	940	2	Q4RGH3_TETNG	Q4rgh3	tetraodon n
1228	153.5	4.9	987	2	Q53MD2_ORYSA	Q53md2	oryza sativ
1229	153.5	4.9	1032	1	TLR9_HUMAN	Q9nr96	homo sapien
1230	153.5	4.9	1041	2	Q9FII5_ARATH	Q9fii5	arabidopsis
1231	153.5	4.9	1110	2	Q9FI77_ARATH	Q9fi77	arabidopsis
1232	153.5	4.9	1121	2	Q942F3_ORYSA	Q942f3	oryza sativ
1233	153.5	4.9	1388	2	Q4RIV6_TETNG	Q4riv6	tetraodon n
1234	153.5	4.9	3247	2	Q65553_9ALPH	Q65553	bovine herp
1235	153.5	4.9	3247	2	Q77CD4_9ALPH	Q77cd4	bovine herp
1236	153	4.9	367	2	Q6GLE8_XENTR	Q6gle8	xenopus tro
1237	153	4.9	529	2	Q5F4C4_CHICK	Q5f4c4	gallus gall
1238	153	4.9	548	2	Q4V8C9_RAT	Q4v8c9	rattus norv
1239	153	4.9	581	2	Q9D5Q5_MOUSE	Q9d5q5	m mus muscu
1240	153	4.9	590	2	Q9D2F4_MOUSE	Q9d2f4	m mus muscu
1241	153	4.9	699	1	VGLG_HHV2H	P13290	human herpe
1242	153	4.9	720	2	Q6PQA5_SPAAU	Q6pqa5	sparus aura
1243	153	4.9	1840	2	Q9ULI4_HUMAN	Q9uli4	homo sapien
1244	153	4.9	2042	1	MDC1_PIG	O76718	sus scrofa
1245	152.5	4.9	163	2	Q6E4F3_PETMA	Q6e4f3	petromyzon
1246	152.5	4.9	370	2	Q5R9V7_PONPY	Q5r9v7	pongo pygma
1247	152.5	4.9	372	2	Q5VZ88_HUMAN	Q5vz88	homo sapien
1248	152.5	4.9	550	2	Q7PT66_ANOGA	Q7pt66	anopheles g
1249	152.5	4.9	577	2	Q8AVI4_XENLA	Q8avi4	xenopus lae
1250	152.5	4.9	581	2	Q9AN90_BRAJA	Q9an90	bradyrhizob
1251	152.5	4.9	585	2	Q89TL5_BRAJA	Q89tl5	bradyrhizob
1252	152.5	4.9	849	1	LAP1_DROME	Q9v780	drosophila
1253	152.5	4.9	1047	2	Q5H719_FUGRU	Q5h719	fugu rubrip
1254	152.5	4.9	1109	2	Q8H4J0_ORYSA	Q8h4j0	oryza sativ
1255	152.5	4.9	1287	2	Q5TMY4_ANOGA	Q5tmy4	anopheles g
1256	152.5	4.9	1295	2	Q8T0X1_BOMMO	Q8t0x1	bombyx mori
1257	152.5	4.9	1356	2	Q8WRE2_ANOGA	Q8wre2	anopheles g
1258	152.5	4.9	1817	2	Q4WMC5_ASPFU	Q4wmc5	aspergillus
1259	152.5	4.9	3288	2	Q7T5D9_CHV1	Q7t5d9	cercopithec
1260	152	4.9	443	1	LRC17_MOUSE	Q9cxd9	mus musculu
1261	152	4.9	562	2	Q9M7W9_ARATH	Q9m7w9	arabidopsis
1262	152	4.8	682	2	Q5JN60_ORYSA	Q5jn60	oryza sativ
1263	152	4.8	776	2	Q6R2K3_ARATH	Q6r2k3	arabidopsis
1264	152	4.8	786	1	TLR1_HUMAN	Q15399	homo sapien
1265	152	4.8	786	2	Q6FI64_HUMAN	Q6fi64	homo sapien
1266	152	4.8	786	2	Q5FWG5_HUMAN	Q5fwg5	homo sapien
1267	152	4.8	796	1	TLR6_HUMAN	Q9y2c9	homo sapien
1268	152	4.8	863	2	Q4R6F0_MACFA	Q4r6f0	macaca fasc
1269	151.5	4.8	347	2	Q9D9Q0_MOUSE	Q9d9q0	mus musculu
1270	151.5	4.8	507	2	Q61X12_CAEBR	Q61x12	caenorhabdi
1271	151.5	4.8	623	2	Q7Q090_ANOGA	Q7q090	anopheles g
1272	151.5	4.8	710	2	Q5TR39_ANOGA	Q5tr39	anopheles g

No.	Score	4.8	Length	Identifier	N	Accession	Organism
1273	151.5	4.8	855	Q8L3Y5_SOYBN	2	Q8L3Y5	glycine max
1274	151.5	4.8	997	Q6K7X5_ORYSA	2	Q6K7X5	oryza sativ
1275	151.5	4.8	998	Q4W9M1_ASPFU	2	Q4W9M1	aspergillus
1276	151.5	4.8	1109	Q84ZJ8_ORYSA	2	Q84ZJ8	oryza sativ
1277	151.5	4.8	1152	Q7PFC4_ANOGA	2	Q7PFC4	anopheles g
1278	151.5	4.8	1152	Q8WRE5_ANOGA	2	Q8WRE5	anopheles g
1279	151.5	4.8	1775	Q54S11_DICDI	2	Q54S11	dictyosteli
1280	151	4.8	163	Q6E4H9_PETMA	2	Q6E4H9	petromyzon
1281	151	4.8	399	Q8BM45_MOUSE	2	Q8BM45	m mus muscu
1282	151	4.8	508	Q50Z76_ENTHI	2	Q50Z76	entamoeba h
1283	151	4.8	530	O08934_MOUSE	2	O08934	mus musculu
1284	151	4.8	540	Q6V6S6_DROSI	2	Q6V6S6	drosophila
1285	151	4.8	540	P93666_HELAN	2	P93666	helianthus
1286	151	4.8	541	Q6V6S8_DROSI	2	Q6V6S8	drosophila
1287	151	4.8	541	Q6V6S9_DROSI	2	Q6V6S9	drosophila
1288	151	4.8	541	Q6V6T0_DROSI	2	Q6V6T0	drosophila
1289	151	4.8	581	O04143_SILLA	2	O04143	silene lati
1290	151	4.8	784	Q6YGU2_RAT	2	Q6YGU2	rattus norv
1291	151	4.8	793	Q704V6_BOVIN	2	Q704V6	bos taurus
1292	151	4.8	793	Q706D2_BOVIN	2	Q706D2	bos taurus
1293	151	4.8	835	TLR4_MOUSE	1	Q9QUK6	mus musculu
1294	151	4.8	835	Q5RGT4_MOUSE	2	Q5RGT4	mus musculu
1295	151	4.8	947	Q8RUT5_ORYSA	2	Q8RUT5	oryza sativ
1296	150.5	4.8	1030	Q8H037_ORYSA	2	Q8H037	oryza sativ
1297	150.5	4.8	1385	Q9VBZ5_DROME	2	Q9VBZ5	drosophila
1298	150.5	4.8	1389	Q24591_DROME	2	Q24591	drosophila
1299	150.5	4.8	289	Q8F3F4_LEPIN	2	Q8F3F4	leptospira
1300	150.5	4.8	329	Q8F115_LEPIN	2	Q8F115	leptospira
1301	150.5	4.8	408	Q8F212_LEPIN	2	Q8F212	leptospira
1302	150.5	4.8	413	Q72TC4_LEPIC	2	Q72TC4	leptospira
1303	150.5	4.8	423	OMD_RAT	2	Q9Z1S7	rattus norv
1304	150.5	4.8	537	Q9C769_ARATH	2	Q9C769	arabidopsis
1305	150.5	4.8	641	Q4TBJ8_TETNG	2	Q4TBJ8	tetraodon n
1306	150.5	4.8	648	Q8BU93_MOUSE	2	Q8BU93	m mus muscu
1307	150.5	4.8	685	Q6AXL3_BRARE	2	Q6AXL3	brachydanio
1308	150.5	4.8	695	FSHR_HUMAN	1	P23945	homo sapien
1309	150.5	4.8	695	Q4QRJ3_HUMAN	2	Q4QRJ3	homo sapien
1310	150.5	4.8	818	Q76CU0_PAROL	2	Q76CU0	paralichthy
1311	150.5	4.8	871	Q5H726_FUGRU	2	Q5H726	fugu rubrip
1312	150.5	4.8	1107	Q8BKP3_MOUSE	2	Q8BKP3	m mus muscu
1313	150.5	4.8	1109	RPK1_IPONI	1	P93194	ipomoea nil
1314	150	4.8	1140	Q91R04_ARATH	2	Q91R04	arabidopsis
1315	150	4.8	1149	Q6GQR9_MOUSE	2	Q6GQR9	mus musculu
1316	150	4.8	1461	Q94H87_ORYSA	2	Q94H87	oryza sativ
1317	150	4.8	1702	Q7PS39_ANOGA	2	Q7PS39	anopheles g
1318	150	4.8	1898	Q62PI4_MOUSE	2	Q62PI4	mus musculu
1319	150	4.8	1944	Q4SlG7_TETNG	2	Q4SlG7	tetraodon n
1320	150	4.8	163	Q6E4E8_PETMA	2	Q6E4E8	petromyzon
1321	150	4.8	239	Q4KP08_LAMAP	2	Q4KP08	lampetra ap
1322	150	4.8	259	LRC3B_HUMAN	1		homo sapien
1323	150	4.8	259	LRC3B_MOUSE	1		mus musculu
1324	150	4.8	259	Q5M8T0_HUMAN	2	Q5M8T0	homo sapien
1325	150	4.8	259	Q543Z7_MOUSE	2	Q543Z7	mus musculu
1326	150	4.8	272	PGS1_PIG	1		sus scrofa
1327	150	4.8	305	Q9N028_MACFA	2	Q9N028	macaca fasc
1328	150	4.8	342	Q4V9E0_BRARE	2	Q4V9E0	brachydanio
1329	150	4.8	348	Q756S8_ASHGO	2	Q756S8	ashbya goss
1330	150	4.8	367	Q86X40_HUMAN	2	Q86X40	homo sapien
1331	150	4.8	584	O49750_ARATH	2	O49750	arabidopsis
1332	150	4.8	594	Q4SDI8_TETNG	2	Q4SDI8	tetraodon n
1333	150	4.8	652	Q8GUM9_ARATH	2	Q8GUM9	arabidopsis
1334	150	4.8	796	Q59HI6_PIG	2	Q59HI6	sus scrofa
1335	150	4.8	802	Q76123_PIG	2	Q76123	sus scrofa
1336	150	4.8	802	Q8LFN2_ARATH	2	Q8LFN2	arabidopsis
1337	150	4.8	803	Q9SRV4_ARATH	2	Q9SRV4	arabidopsis
1338	150	4.8	1294	Q8RZV7_ORYSA	2	Q8RZV7	oryza sativ
1339	150	4.8	1305	TCGAP_MOUSE	1		mus musculu
1340	150	4.8	1315	CHAO_DROME	1	P12024	drosophila
1341	149.5	4.8	98	Q90XG3_CHICK	1	Q90XG3	gallus gall
1342	149.5	4.8	163	Q6E4E9_PETMA	2	Q6E4E9	petromyzon
1343	149.5	4.8	164	Q6E4G8_PETMA	2	Q6E4G8	petromyzon
1344	149.5	4.8	167	Q6E4I1_PETMA	2	Q6E4I1	petromyzon
1345	149.5	4.8	224	O44086_CAEEL	2	O44086	caenorhabdi
1346	149.5	4.8	542	Q6V4C6_DROYA	2	Q6V4C6	drosophila
1347	149.5	4.8	657	Q6L569_ORYSA	2	Q6L569	oryza sativ
1348	149.5	4.8	696	Q9DGF5_CYNPY	2	Q9DGF5	cynops pyrr
1349	149.5	4.8	894	Q8GYR8_ARATH	2	Q8GYR8	arabidopsis
1350	149.5	4.8	957	Q9SRL2_ARATH	2	Q9SRL2	arabidopsis
1351	149.5	4.8	1056	Q7XFM6_ORYSA	2	Q7XFM6	oryza sativ
1352	149.5	4.8	1056	Q8S7A6_ORYSA	2	Q8S7A6	oryza sativ
1353	149.5	4.8	1469	Q51AW9_ENTHI	2	Q51AW9	entamoeba h
1354	149.5	4.8	1791	Q4P4A9_USTMA	2	Q4P4A9	ustilago ma
1355	149	4.8	167	Q6E4D3_PETMA	2	Q6E4D3	petromyzon
1356	149	4.8	295	Q86DD0_CAEEL	2	Q86DD0	caenorhabdi
1357	149	4.8	310	Q86S81_CAEEL	2	Q86S81	caenorhabdi
1358	149	4.8	341	Q9N5D7_CAEEL	2	Q9N5D7	caenorhabdi
1359	149	4.8	366	Q7QHQ2_ANOGA	2	Q7QHQ2	anopheles g
1360	149	4.8	375	Q9N4Z5_CAEEL	2	Q9N4Z5	caenorhabdi
1361	149	4.8	421	Q7PNQ0_ANOGA	2	Q7PNQ0	anopheles g
1362	149	4.8	437	Q7Q6S9_ANOGA	2	Q7Q6S9	anopheles g
1363	149	4.8	471	Q9LRV8_ARATH	2	Q9LRV8	arabidopsis
1364	149	4.8	763	Q4Q5Q5_LEIMA	2	Q4Q5Q5	leishmania
1365	149	4.8	784	TLR2_CRIGR	1		cricetulus
1366	149	4.8	927	Q8N537_HUMAN	2	Q8N537	homo sapien
1367	149	4.8	972	Q5AXH5_EMENI	2	Q5AXH5	aspergillus
1368	149	4.8	1025	Q40640_ORYSA	2	Q40640	oryza sativ
1369	149	4.8	1025	Q7DMC2_ORYLO	2	Q7DMC2	oryza longi
1370	149	4.8	1143	BRL2_ARATH	2	Q9ZPS9	arabidopsis
1371	149	4.8	1164	Q53JZ9_ORYSA	2	Q53JZ9	oryza sativ
1372	149	4.8	1504	Q9UES6_HUMAN	2	Q9UES6	homo sapien
1373	149	4.8	1504	Q6PIB4_HUMAN	2	Q6PIB4	homo sapien
1374	149	4.8	1504	Q7Z2X6_HUMAN	2	Q7Z2X6	homo sapien
1375	149	4.8	1504	Q6PGP3_HUMAN	2	Q6PGP3	homo sapien
1376	149	4.8	1522	O15069_HUMAN	2	O15069	homo sapien
1377	149	4.8	1528	Q9Y2I1_HUMAN	2	Q9Y2I1	homo sapien
1378	149	4.8	1874	Q75F93_ASHGO	2	Q75F93	ashbya goss
1379	149	4.8	2357	Q86S1_DICDI	2	Q86S1	dictyosteli
1380	149	4.8	2357	Q9U1M8_DICDI	2	Q9U1M8	dictyosteli
1381	148.5	4.7	163	Q6E4F7_PETMA	2	Q6E4F7	petromyzon
1382	148.5	4.7	215	Q91VH8_MOUSE	2	Q91VH8	mus musculu
1383	148.5	4.7	232	Q5T508_HUMAN	2	Q5T508	homo sapien
1384	148.5	4.7	321	Q6X8P9_BOVIN	2	Q6X8P9	bos taurus
1385	148.5	4.7	375	FMOD_BOVIN	1	P13605	bos taurus
1386	148.5	4.7	376	FMOD_RAT	1	P50609	rattus norv
1387	148.5	4.7	516	Q4T9I8_TETNG	2	Q4T9I8	tetraodon n
1388	148.5	4.7	610	Q21604_CAEEL	2	Q21604	caenorhabdi
1389	148.5	4.7	646	Q8PQD3_XANAC	2	Q8PQD3	xanthomonas
1390	148.5	4.7	680	Q93374_CAEEL	2	Q93374	caenorhabdi
1391	148.5	4.7	687	Q61PG2_CAEBR	2	Q61PG2	caenorhabdi
1392	148.5	4.7	695	FSHR_MACFA	1	P32212	macaca fasc
1393	148.5	4.7	807	Q6GPJ8_XENLA	2	Q6GPJ8	xenopus lae
1394	148.5	4.7	890	Q9LQl1_ARATH	2	Q9LQl1	arabidopsis
1395	148.5	4.7	964	Q8VYT7_ARATH	2	Q8VYT7	arabidopsis
1396	148.5	4.7	964	Q9LY03_ARATH	2	Q9LY03	arabidopsis
1397	148.5	4.7	1013	Q96PY9_HUMAN	2	Q96PY9	homo sapien
1398	148.5	4.7	1016	Q9LRT1_ARATH	2	Q9LRT1	arabidopsis
1399	148.5	4.7	1099	Q8WXE4_HUMAN	2	Q8WXE4	homo sapien
1400	148.5	4.7	1115	GR101_LYMST	1	P46023	lymnaea sta
1401	148.5	4.7	1140	Q7S718_NEUCR	2	Q7S718	neurospora
1402	148.5	4.7	1279	Q4RJ85_TETNG	2	Q4RJ85	tetraodon n
1403	148	4.7	311	Q8F116_LEPIN	2	Q8F116	leptospira
1404	148	4.7	338	LUM_RAT	1	P51886	rattus norv
1405	148	4.7	449	Q4SR98_TETNG	2	Q4SR98	tetraodon n
1406	148	4.7	572	Q72S79_LEPIC	2	Q72S79	leptospira
1407	148	4.7	581	Q505F5_MOUSE	2	Q505F5	mus musculu
1408	148	4.7	592	Q4REF6_TETNG	2	Q4REF6	tetraodon n
1409	148	4.7	724	Q651V0_ORYSA	2	Q651V0	oryza sativ
1410	148	4.7	745	Q89X06_BRAJA	2	Q89X06	bradyrhizob
1411	148	4.7	811	Q59HI5_PIG	2	Q59HI5	sus scrofa
1412	148	4.7	811	Q4LDR6_PIG	2	Q4LDR6	sus scrofa
1413	148	4.7	915	Q5SMW5_ORYSA	2	Q5SMW5	oryza sativ
1414	148	4.7	1095	Q6URA2_9ROSA	2	Q6URA2	malus bacca
1415	148	4.7	1188	Q41805_MAIZE	2	Q41805	zea mays (m
1416	148	4.7	1964	NOTC4_MOUSE	1	P31695	mus musculu
1417	148	4.7	2143	Q75T35_GLOLA	2	Q75T35	glomerella
1418	147.5	4.7	163	Q6E4M8_PETMA	2	Q6E4M8	petromyzon

1419	147.5	4.7	316	1	PGLB_CHICK	Q90944 gallus gall
1420	147.5	4.7	370	1	LRC19_HUMAN	Q9H756 homo sapien
1421	147.5	4.7	370	2	S53GE4_HUMAN	Q53ge4 homo sapien
1422	147.5	4.7	376	1	FMOD_MOUSE	P50608 mus musculu
1423	147.5	4.7	376	2	Q543D2_MOUSE	Q543d2 m 0 day neo
1424	147.5	4.7	376	2	Q8BNU3_MOUSE	Q8bnu3 mus musculu
1425	147.5	4.7	404	2	Q7TPZ1_MOUSE	Q7tpz1 mus musculu
1426	147.5	4.7	416	2	Q4TB58_TETNG	Q4tb58 tetraodon n
1427	147.5	4.7	499	2	Q8VYG9_ARATH	Q8vyg9 arabidopsis
1428	147.5	4.7	541	2	Q6V6S5_DROSI	Q6v6s5 drosophila
1429	147.5	4.7	557	2	Q53P27_ORYSA	Q53p27 oryza sativ
1430	147.5	4.7	570	2	Q4QGK0_LEIMA	Q4qgk0 leishmania
1431	147.5	4.7	646	2	Q83XD4_9XANT	Q83xd4 xanthomonas
1432	147.5	4.7	673	2	Q5EBP4_MOUSE	Q5ebp4 mus musculu
1433	147.5	4.7	903	2	Q51YX1_MAGGR	Q51yx1 magnaporthe
1434	147.5	4.7	964	2	Q8L3T4_ORYSA	Q8l3t4 oryza sativ
1435	147.5	4.7	1005	2	Q5JPC9_HUMAN	Q5jpc9 homo sapien
1436	147.5	4.7	1052	2	Q6K2G4_ORYSA	Q6k2g4 oryza sativ
1437	147.5	4.7	1099	2	Q8N1F8_HUMAN	Q8n1f8 homo sapien
1438	147.5	4.7	1194	2	Q6PCM6_MOUSE	Q6pcm6 mus musculu
1439	147.5	4.7	1248	2	Q54XZ5_DICDI	Q54xz5 dictyosteli
1440	147.5	4.7	1385	2	Q7JPR9_DROME	Q7jpr9 drosophila
1441	147.5	4.7	2157	1	BAT2_HUMAN	P48634 homo sapien
1442	147	4.7	224	1	Q5EI81_PIG	Q5ei81 sus scrofa
1443	147	4.7	238	1	Q4TBU2_TETNG	Q4tbu2 tetraodon n
1444	147	4.7	272	2	Q72ND5_LEPIC	Q72nd5 leptospira
1445	147	4.7	388	2	Q9DDZ9_PETMA	Q9ddz9 petromyzon
1446	147	4.7	498	2	Q8F3F9_LEPIN	Q8f3f9 leptospira
1447	147	4.7	519	2	Q7Q548_ANOGA	Q7q548 anopheles g
1448	147	4.7	526	2	Q84GT9_YEREN	Q84gt9 yersinia en
1449	147	4.7	686	2	Q4SEN4_TETNG	Q4sen4 tetraodon n
1450	147	4.7	835	2	Q8K2T5_MOUSE	Q8k2t5 mus musculu
1451	147	4.7	960	2	Q6K7T8_ORYSA	Q6k7t8 oryza sativ
1452	147	4.7	1118	2	Q76CZ4_HORVU	Q76cz4 hordeum vul
1453	147	4.7	1118	2	Q76CZ5_HORSP	Q76cz5 hordeum spo
1454	147	4.7	1118	2	Q76CZ6_HORVU	Q76cz6 hordeum vul
1455	147	4.7	2414	2	EP300_HUMAN	Q09472 homo sapien
1456	147	4.7	2805	1	MAP1A_HUMAN	P78559 homo sapien
1457	146.5	4.7	245	2	Q4TO4_TETNG	Q4to4 tetraodon n
1458	146.5	4.7	325	2	Q8NAB7_HUMAN	Q8nab7 homo sapien
1459	146.5	4.7	382	2	Q9SZH9_ARATH	Q9szh9 arabidopsis
1460	146.5	4.7	383	2	Q8RWE5_ARATH	Q8rwe5 arabidopsis
1461	146.5	4.7	409	2	Q6P3D8_MOUSE	Q6p3d8 mus musculu
1462	146.5	4.7	438	2	Q7WA81_BORPA	Q7wa81 bordetella
1463	146.5	4.7	508	1	AMGO3_RAT	Q80zd5 rattus norv
1464	146.5	4.7	521	2	Q62PW2_MOUSE	Q62pw2 mus musculu
1465	146.5	4.7	524	1	Q6DJK2_XENLA	Q6djk2 xenopus lae
1466	146.5	4.7	536	2	Q4QGI4_LEIMA	Q4qgi4 leishmania
1467	146.5	4.7	629	2	Q4QGJ0_LEIMA	Q4qgj0 leishmania
1468	146.5	4.7	675	2	Q80WJ1_MOUSE	Q80wj1 mus musculu
1469	146.5	4.7	717	2	Q7F1K6_ORYSA	Q7f1k6 oryza sativ
1470	146.5	4.7	776	2	Q4QGM1_LEIMA	Q4qgm1 leishmania
1471	146.5	4.7	832	2	Q4S150_TETNG	Q4s150 tetraodon n
1472	146.5	4.7	861	2	Q69JZ8_ORYSA	Q69jz8 oryza sativ
1473	146.5	4.7	906	2	Q6QNU9_MOUSE	Q6qnu9 mus musculu
1474	146.5	4.7	925	2	Q9SIX4_ARATH	Q9six4 arabidopsis
1475	146.5	4.7	950	2	Q8MQN5_DROME	Q8mqn5 drosophila
1476	146.5	4.7	1016	2	Q9SPM0_MAIZE	Q9spm0 zea mays (m
1477	146.5	4.7	1122	2	Q5BDB8_EMENI	Q5bdb8 aspergillus
1478	146.5	4.7	1128	2	Q5ZBC0_ORYSA	Q5zbc0 oryza sativ
1479	146.5	4.7	1404	1	SERR_DROME	P18168 drosophila
1480	146.5	4.7	1439	2	Q88NY1_PSEPK	Q88ny1 pseudomonas
1481	146.5	4.7	1860	2	Q8IZC6_HUMAN	Q8izc6 homo. sapien
1482	146	4.7	369	2	Q91332_PSEAE	Q91332 pseudomonas
1483	146	4.7	661	2	Q8C251_MOUSE	Q8c251 mus musculu
1484	146	4.7	673	2	Q6K0L4_BOTJA	Q6k0l4 bothrops ja
1485	146	4.7	785	2	Q9LVN2_ARATH	Q9lvn2 arabidopsis
1486	146	4.7	788	2	O18510_TRINI	O18510 trichoplusi
1487	146	4.7	827	2	Q6R0H4_MOUSE	Q6r0h4 mus musculu
1488	146	4.7	876	2	Q6R0H5_MOUSE	Q6r0h5 mus musculu
1489	146	4.7	942	2	Q5N7Z4_ORYSA	Q5n7z4 oryza sativ
1490	146	4.7	1133	2	Q6R0H7_MOUSE	Q6r0h7 mus musculu
1491	146	4.7	1173	2	Q9FL28_ARATH	Q9fl28 arabidopsis

1492	146	4.7	1413	2	Q7F8Q9_ORYSA	Q7f8q9 oryza sativ
1493	146	4.7	1536	2	Q4P7T7_USTMA	Q4p7t7 ustilago ma
1494	145.5	4.6	167	2	Q6B4F4_PETMA	Q6b4f4 petromyzon
1495	145.5	4.6	352	2	Q7XNY1_ORYSA	Q7xny1 oryza sativ
1496	145.5	4.6	373	1	Q4SR97_TETNG	Q4sr97 tetraodon n
1497	145.5	4.6	380	1	FMOD_CHICK	P51887 gallus gall
1498	145.5	4.6	687	1	FSHR_EQUAS	Q95179 equus asinu
1499	145.5	4.6	807	2	O18511_TRINI	O18511 trichoplusi
1500	145.5	4.6	827	2	Q6ZG00_ORYSA	Q6zg00 oryza sativ

ALIGNMENTS

RESULT 1

Q6UXL5_HUMAN

ID   Q6UXL5_HUMAN PRELIMINARY;   PRT;   598 AA.
AC   Q6UXL5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CSRV314.
GN   ORFNames=UNQ314;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358298; AAQ88665.1; -; mRNA.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00560; LRR_1; 3.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00369; LRR_TYP; 5.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS50853; FN3; 1.
SQ   SEQUENCE   598 AA;   63029 MW; C596CBE963AA86C CRC64;

Query Match   100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity   100.0%; Pred. No. 1.2e-168;
Matches 598; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF   60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF   60

Qy   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE  120

Qy  121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL  180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL  180

Qy  181 RPEDLAGLAALQBLDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 RPEDLAGLAALQBLDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE  240

Qy  241 SHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL   300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 SHVTLASPEETRCHFPPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL  300

Qy  301 APTWLSPTPAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 APTWLSPTPAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEG 360

Qy  361 FTGLYCESQMGGQTRPSPTPVTPRPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR   420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 FTGLYCESQMGGQTRPSPTPVTPRPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR   420

Qy  421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT  480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHT  480

Qy  481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540

Qy  541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPFPGPGPGLQSPLHAKPYI 598
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPFPGPGPGLQSPLHAKPYI 598
```

RESULT 2
Q6UXL4_HUMAN
ID   Q6UXL4_HUMAN PRELIMINARY;   PRT;   673 AA.
AC   Q6UXL4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   CSRV314 (Slit-like 2).
GN   Name=SLITL2; ORFNames=UNQ314;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.

RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta.
RG   NIH MGC Project;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY358299; AAQ88666.1; -; mRNA.
DR   EMBL; BC068575; AAH68575.1; -; mRNA.
DR   Ensembl; ENSG00000168140; Homo sapiens.
DR   InterPro; IPR000422; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR003885; LRR_Cyst.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 6.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00365; LRR_SD22; 4.
DR   SMART; SM00369; LRR_TYP; 8.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00026; EGF_3; 1.
DR   PROSITE; PS50853; FN3_1.
SQ   SEQUENCE 673 AA; 71655 MW; 4CDFA39121D4BF8 CRC64;

Query Match   98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity   88.7%; Pred. No. 1.1e-165;
Matches 597; Conservative   0; Mismatches   0; Indels   1; Gaps 1;

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Qy    1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF    60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MCSRVPLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF    60

Qy   61 ENGITMLDASSFAGLPGLQLLDLSQNQIAS----------------------------   90
        |||||||| ||||||||||||||||||||||
Db   61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy   91 -------------------------------------------LRIPRLLLLDLSHNS   105
                                                   |||||||||||||||
Db  121 RGLRLRERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS 180

Qy  106 LLALEPGILDTANVEALRLAGLAGLQLQLDEGLFSRLRNLHDLDVSDNQLERVPVIRGLRG 165
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  ...
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DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00560; LRR 1; 6.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00365; LRR_SD22; 4.
DR   SMART; SM00369; LRR_TYP; 8.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS50853; FN3; 1.
SQ   SEQUENCE   673 AA;  71712 MW;  891E149652DEA286 CRC64;

Query Match             98.2%;  Score 3078.5;  DB 2;  Length 673;
Best Local Similarity   88.6%;  Pred. No. 2e-165;
Matches  596;  Conservative    0;  Mismatches    0;  Indels   75;  Gaps    1;

Qy   1  MCSRVPLLLPLLLLLALGPGVQGCPSGGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  MCSRVPLLLPLLLLLALGPGVQGCPSGGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF  60

Qy  61  ENGITMLDASSFAGLPGLQLLDLSQNQIAS                                90
        ||||||||.|||||||||||||||||||||
Db  61  ENGITMLDAGSFAGLPGLQLLDLSQNQIASLSPSGVFQPLANLSNLDLTANRLHEITNETF 120

Qy  91  ------------------------------------LRLPRLLLLDLSHNS           105
                                            |||||||||||||||
Db 121  RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS  180

Qy 106  LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  165
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181  LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRG  240

Qy 166  LTRLRLAGNTRIAQLRPEDLAGLAGLGLQQLDSGLFPRLRLLAAARNPF            225
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 241  LTRLRLAGNTRIAQLRPEDLAGLAGLGLQQLDSGLFPRLRLLAAARNPF            300

Qy 226  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT  285
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301  NCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPT  360

Qy 286  TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC  345
        |||||||||||||||||||||||.||||||||||||||||||||||||||||||||||
Db 361  TRPVVREPTALSSSLAPTWLSPTEPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTC  420

Qy 346  HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTTLGIEPVSPTSLRVGL 405
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421  HLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTTLGIEPVSPTSLRVGL 480

Qy 406  QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP  465
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481  QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP  540

Qy 466  GRVPEGBEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR  525
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541  GRVPEGBEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR  600

Qy 526  RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG  585
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601  RGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG  660

Qy 586  PGLQSPLHAKPYI  598
        |||||||||||||
Db 661  PGLQSPLHAKPYI  673
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Qy   91 ---------------------------------------------------------LRLPRLLLDLSHNSLLALEPGILDTA 117
                                                                 ||||||||||||||||||||||||||
Db   61 KNRIRHIQPGAFDTLDRLLEKLLQDNELRALPLRLPRLLLDLSHNSLLALEPGILDTA 120

Qy  118 NVEALRLAGLGLQLQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRI 177
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 NVEALRLAGLGLQLQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRI 180

Qy  178 AQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPNCVCPLSWFGPW 237
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPNCVCPLSWFGPW 240

Qy  238 VRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS 297
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS 300

Qy  298 SSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLC 357
         |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SSLAPTWLSPTEPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLC 360

Qy  358 PEGFTGLYCESQMGQGTRPSPTPVTRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLR 417
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 PEGFTGLYCESQMGQGTRPSPTPVTRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLR 420

Qy  418 SLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGE 477
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 SLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGE 480

Qy  478 AHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDK 537
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDK 540

Qy  538 GQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPY 597
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPY 600

Qy  598 I 598
         |
Db  601 I 601
```

DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   SLITL2 protein (Fragment).
GN   Name=SLITL2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013767; AAH13767.1; -; mRNA.
DR   HSSP; Q9BZR6; 1P8T.
DR   Ensembl; ENSG00000168140; Homo sapiens.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001611; FN_III.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR003961; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00560; LRR; 6.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00369; LRR_TYP; 2.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50026; EGF_3; 1.
DR   PROSITE; PS50853; FN3; 1.
KW   EGF-like domain; Leucine-rich repeat.
FT   NON_TER   1   1
SQ   SEQUENCE   601 AA; 64178 MW; 496407F778D9ABD2 CRC64;

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Query Match             86.0%;  Score 2697.5;  DB 2;  Length 601;
Best Local Similarity   87.4%;  Pred. No. 5.4e-144;
Matches  525;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy   73 AGLPGLQLLDLSQNQIAS--------------------------------------------- 90
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Db    1 AGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFGRLRRLERLYLG 60
```

RESULT 5
Q8BJ0_MOUSE
ID   Q8BJ0_MOUSE PRELIMINARY;   PRT;   673 AA.
AC   Q8BJ0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
DE   library, clone:D030066D07 product:hypothetical Prokaryotic membrane
DE   lipoprotein lipid attachment site/Cysteine-rich flanking region, N-
DE   terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich repeat,
DE   typical subtype/Leucine-rich repeat, outliers/Cysteine-rich flanking
DE   region, C-terminal/Leucine-rich region/Fibronectin type III domain
DE   containing protein, full insert sequence.
GN   Name=Slitl2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44 (1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RC   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro M., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami S., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK083684; BAC38992.1; -; mRNA.
DR   HSSP; P00740; 1EDM.
DR   MGI; MGI:2177651; Slit12.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001611; LRR.

DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00560; LRR; 6.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00369; LRR_TYP; 3.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00026; EGF_3; 1.
DR   PROSITE; PS00853; FN3; 1.
KW   Hypothetical protein; Lipoprotein.
SQ   SEQUENCE   673 AA; 72284 MW; E35D1B35DDFF5EDB CRC64;

Query Match   79.5%; Score 2491; DB 2; Length 673;
Best Local Similarity   73.5%; Pred. No.2.6e-132;
Matches 491; Conservative 25; Mismatches 74; Indels 78; Gaps 3;

Qy   6 PLLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT   65
              ||| | |||||| ||| |||||||||||||||||||||||||||||||||||||
Db   9 PLL--LLLIVLLGSGVQGCPSGCQCNQPQTVFCTARQGTTVPRDVPPDTVGLYIFENGIT   66

Qy   66 MLDASSFAGLPGLQLLDLSQNQIAS-------------------------------------   90
              |||||||
Db   67 TLDVGCFAGLPGLQLLDLSQNQTSLPGGIFQPLVNLSNLDLTANKLHEISNETFRGLRR   126

Qy   91 -------------------------------LRLPRLLLLDLSHNSLLALE   110
                                           |||||||||| ||||||||||
Db   127 LERLYLGKNRIRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHNSIPALE   186

Qy   111 PGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLLDVSDNQLERVPPVIRGLRGLTRLR   170
              |||||||||||||||||| ||||||||||||||||||||||| | ||||||||||
Db   187 AGILDTANVEALRLAGLGLRQLDEGLFGRLLNLHDLLDVSDNQLEHMPSVIQGLRGLTRLR   246

Qy   171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCP   230
              ||||||||| |||||||||||||||||||| |||||||| |||||||||||||||||| |
Db   247 LAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNPFNCLCP   306

Qy   231 LSWFGPWVRESHVTLASPEETRCHFPPKQNAGRLLLELDYADFGCPATTTATVPTTRPVV   290
              ||||||| ||| ||||||||||||||||||||||| |||||| ||| ||||||||||||
Db   307 LSWFGPWVRENHVVLASPEETRCHFPPKQNAGRLLLDLDYADFGCPVTTTATVPTIRSTI   366

Qy   291 REPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTR   350
              | | | | || ||||| | ||||| ||||| |||||| | || ||| | |
Db   367 RBPTLSTSSQAPTWPSHTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGSCRLGAR   426

Qy   351 HHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQ   410
              || |||||||| ||||| | ||| || | || || |||||||||||| |||||||
Db   427 HHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPLLPLSIEPVSPTSLRVKLQRYLQ   486

Qy   411 GSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPE   470
              | ||||||||||||||||||||||||||||||||||||||||||| |||| || || |
Db   487 GNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPE   546

Qy   471 GEBACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAM   530
              |||||| || | |||||| ||||||||||||||| ||||| | ||||| | || ||
Db   547 GEBACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCVRRARA-   605

Qy   531 AAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGGSECEVPLMGFPPGPGLQS   590
              : | | || | |||||| || | |||| ||||||||| || ||||||| |||| |
Db   606 TSTAQDKGQVGPGTGPLELEGVKAPLEPGSGPECEVPLMGYVPGPSLQG   665

Qy   591 PLHAKPYI 598
              || |||||
Db   666 VLPAKHYI 673

```
RESULT 6
Q8R2G5_MOUSE
ID   Q8R2G5_MOUSE PRELIMINARY;      PRT;   673 AA.
AC   Q8R2G5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Slit-like 2 protein precursor.
GN   Name=Slitl2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6;
RA   Schrewe H., Kutejova E.;
RT   "Structure and expression analysis of the mouse Slit-like 2 (Slitl2)
RT   gene.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RG   Director MGC Project;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ458938; CAD30331.1; -; mRNA.
DR   EMBL; BC050274; AAH50274.1; -; mRNA.
DR   HSSP; P00740; 1EDM.
DR   Ensembl; ENSMUSG00000039646; Mus musculus.
DR   MGI; MGI:2177651; Slitl2.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00560; LRR_1; 6.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00369; LRR_TYP; 3.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00026; EGF_3; 1.
DR   PROSITE; PS50853; FN3; 1.
KW   Signal.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    673       Slit-like 2 protein.
SQ   SEQUENCE   673 AA;  72260 MW;  AAB8DA82DA8E9D32 CRC64;

Query Match             79.4%;  Score 2490;  DB 2;  Length 673;
Best Local Similarity   73.5%;  Pred. No. 3e-132;
Matches  491;  Conservative  25;  Mismatches  74;  Indels  78;  Gaps  3;

Qy      6 PLLLPLLLLALGPGVQGCPSGGCQCSQPQTVFCTARQGTVPRDVPPDTVGLYVFENGIT 65
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Db      9 PLL--LLLLVLLGGSGVQGCPSGGCQCNQPQTVFCTARQGTVPRDVPPDTVGLYIFENGIT 66

Qy     66 MLDASSFAGLPGLQLLDLSQNQIAS----------------------------------- 90
            |||||||||||||||||||||||
Db     67 TLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNETFRGLRR 126

Qy     91 ------------------------------------LRLPRLLLLDLSHNSLLALE 110
                                                ||:|||||||||||||||||||
Db    127 LERLYLGKNRIRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHNSIPALE 186

Qy    111 PGILDTANVEALRLAGLGLQQLDEGLFSRLRLNLHDLDVSDNQLERVPVIRGLRGLTRLR 170
            |||||||||||||||||||||||||||||| :|||:|||||||||| |||||||||||||
Db    187 AGILDTANVEALRLAGLGLQRLDEGLFGRLLNLHDLDVSDNQLEHMPSVIQGLRGLTRLR 246

Qy    171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPENCVCP 230
            ||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||||:|
Db    247 LAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNPENCLCP 306

Qy    231 LSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVV 290
            ||||||||||| ||||||||||||||||||||||||||||||||||||| ||||||:|||
Db    307 LSWFGPWVRENHVVLASPEETRCHFPPKNAGRLLLDLDYADFGCPVTTTTATVPTIRSTI 366

Qy    291 REPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTR 350
            ||||:| |||||| |||||:| ||||||||||||:||:||||||:|||||||||||||||
Db    367 REPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRAPAPQPQDCPASICLNGGSCRLGAR 426

Qy    351 HHLACLCPEGFTGLYCESQMGCQTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQ 410
            ||| ||||||||||||||| ||::|:| :|| ||||||:||||||||||||:|||||||||
Db    427 HHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPLPLSIEPVSPTSLRVKLQRYLQ 486

Qy    411 GSSVQLRSLRLITYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPE 470
            |:|||||||||| |||||||||||||||||||||||||||||||||||||:|:||||||
Db    487 GNTVQLRSLRLITYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPE 546

Qy    471 GEEACGRAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAVCVRRGRAM 530
            ||||| :||| ||||||||||||||||||||||||||||||||| :||||||||||||
Db    547 GEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCVRRARA- 605

Qy    531 AAAAQDKGQVGPGAGPLELEGVKVPLEPGKATEGGGEALPSGSECEVPLMGFPGPGLQS 590
            :|  ||||||||| |||||||||||||:|||||||||| ||||:|||||||||||||||
Db    606 TSTAQDKGQVGPGTGPLELEGVKAPLEPGSKATEGGGEALSGGPECEVPLMGYPGPSLQG 665

Qy    591 PLHAKPYI 598
            | ||||||
Db    666 VLPAKHYI 673


RESULT 7
Q9CZT5_MOUSE
ID   Q9CZT5_MOUSE PRELIMINARY;      PRT;   673 AA.
AC   Q9CZT5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE   enriched library, clone:2610528G05 product:hypothetical Prokaryotic
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DE    membrane lipoprotein lipid attachment site/Cysteine-rich flanking
DE    region, N-terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich
DB    repeat, typical subtype/Leucine-rich repeat, outliers/Cysteine-rich
DB    flanking region, C-terminal/Leucine-rich region/Fibronectin type III
DB    domain containing protein, full insert sequence.
GN    Name=Slit2;
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC    Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6J; TISSUE=Whole body;
RX    MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA    Carninci P., Hayashizaki Y.;
RT    "High-efficiency full-length cDNA cloning.";
RL    Meth. Enzymol. 303:19-44(1999).
RN    [2]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6J; TISSUE=Whole body;
RX    MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA    Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA    Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA    Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA    Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA    Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA    Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA    Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA    Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA    Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA    Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA    Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA    Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA    Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA    Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA    Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA    Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA    Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA    Hayashizaki Y.;
RT    "Functional annotation of a full-length mouse cDNA collection.";
RL    Nature 409:685-690(2001).
RN    [3]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6J; TISSUE=Whole body;
RA    The FANTOM Consortium;
RT    "Analysis of the mouse transcriptome based on functional annotation of
RT    60,770 full-length cDNAs.";
RL    Nature 420:563-573(2002).
RN    [4]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6J; TISSUE=Whole body;
RX    MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA    Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA    Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT    "Normalization and subtraction of cap-trapper-selected cDNAs to
RT    prepare full-length cDNA libraries for rapid discovery of new genes.";
RL    Genome Res. 10:1617-1630(2000).
RN    [5]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6J; TISSUE=Whole body;
RX    MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA    Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA    Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA    Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA    Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA    Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA    Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsuura S., Kawai J.,
RA    Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT    "RIKEN integrated sequence analysis (RISA) system-384-format
RT    sequencing pipeline with 384 multicapillary sequencer.";
RL    Genome Res. 10:1757-1771(2000).
RN    [6]
RP    NUCLEOTIDE SEQUENCE.
RC    STRAIN=C57BL/6J; TISSUE=Whole body;
RA    Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA    Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA    Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA    Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA    Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA    Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA    Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA    Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA    Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA    Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.;
RL    Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AK012169; BAB28075.1; -; mRNA.
DR    HSSP; P00740; 1EDM.
DR    Ensembl; ENSMUSG00000039646; Mus musculus.
DR    MGI; MGI:2177651; Slit2.
DR    InterPro; IPR000742; EGF_2.
DR    InterPro; IPR006209; EGF_like.
DR    InterPro; IPR003961; FN_III.
DR    InterPro; IPR006210; IEGF.
DR    InterPro; IPR001611; LRR.
DR    InterPro; IPR000483; LRR_Cterm.
DR    InterPro; IPR000372; LRR_Nterm.
DR    InterPro; IPR003591; LRR_typ.
DR    Pfam; PF00008; EGF; 1.
DR    Pfam; PF00041; fn3; 1.
DR    Pfam; PF01463; LRRCT; 1.
DR    Pfam; PF01462; LRRNT; 1.
DR    Pfam; PF05560; LRR_1; 6.
DR    PRINTS; PR00019; LEURICHRPT.
DR    SMART; SM00181; EGF; 1.
DR    SMART; SM00060; FN3; 1.
DR    SMART; SM00082; LRRCT; 1.
DR    SMART; SM00013; LRRNT; 1.
DR    SMART; SM00369; LRR_TYP; 3.
DR    PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR    PROSITE; PS01186; EGF_2; 1.
DR    PROSITE; PS50026; EGF_3; 1.
DR    PROSITE; PS50853; FN3_1; 1.
KW    Hypothetical protein; Lipoprotein.
SQ    SEQUENCE   673 AA;  72336 MW;  9C53F90ADF43FBD9 CRC64;

Query Match             79.2%;  Score 2484;  DB 2;  Length 673;
Best Local Similarity   73.4%;  Pred. No. 6.6e-112;
Matches  490;  Conservative  25;  Mismatches  75;  Indels  78;  Gaps  3;

Qy      6 PLLPLLLLALGPGVGGCPSGCQCSOPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT 65
          | ||: |||||||| ||||||||||||||||||||||||||||||||:||||||||||||
Db      9 PLL-LLLVLLGSGVGGCPSGCQCNQPQTVFCTARQGTTVPRDVPPDTVGLYIFENGIT 66

Qy     66 MLDASSFAGLPGLQLLDLSQNOIAS                                  90
          |||||||||||||||||
Db     67 TLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNETFRGLRR 126

Qy     91 ---------------------LRLPRLLLLDLSHNSLLALE 110
                               |||||||||:|||||||||||||
Db    127 LERLYLGKNRIRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHNSIPALE 186

Qy    111 PGILDTANVEALRLAGLGLQLQDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRTLRLR 170
          ||||||||||||||||||||||:||||||:|||||||||||||:|||:|||||||||||
Db    187 AGILDTANVEALRLAGLGLRQLDEGLFGRLLNLHDLDVYDNQLEHMPSVIQGLRGLTRLR 246

Qy    171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLLAAARNPFNCVCP 230
          |||||||||||||||||||||||||:||||||||||||||||||||||||||||||||:|
Db    247 LAGNTRIAQIRPEDLAGLTALQELDVSNLSQALPSDLSSLFPRLRLLAAARNPFNCLCP 306

Qy    231 LSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTVPTTRPVV 290
          |||||||||::|||||||||||||||||||||||||||||||||||:|||: :
Db    307 LSWFGPWVRENHVLASPEETRCHFPPKNAGRLLLLDLDYADFGCPVTTTATVPTIRSTI 366
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Qy  291  REPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTR  350
         ||||:||:||||| ||| |  |:||:| |:||||||||||||||||:   |||||:|||||
Db  367  REPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGSCRLGAR  426

Qy  351  HHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTTLGIEPVSPTSLRVGLQRYLQ  410
         || .||||||.|||||||    |  || ||  ||||| |   |||||||||||| |||||||
Db  427  HHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPLLPLPLSIEPVSPTSLRVKLQRYLQ  486

Qy  411  GSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPE  470
         |:.|||||||||||||||||||||||||||||||||||||||||||:||.|||.||.|||
Db  487  GNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLGAGRTPE  546

Qy  471  GEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAM  530
         ||||||||:| .|.|||||||||||||||||||||||||||| ||||.|||||||| ||
Db  547  GEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCVRRARA-  605

Qy  531  AAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPCLQS  590
         :|:||||||||||:|||||||||.|||||||||||||||| :|:| |||||||:|||.||:
Db  606  TSTAQDKGQVGPGTGPLELEGVKAPLEPGPKATEGGGEALSGSGPECEVPLMGYPGPSLQG  665

Qy  591  PLHAKPYI  598
         .| ||:||
Db  666  VLPAKHYI  673
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RESULT 8
Q6DF55_XENTR
ID   Q6DF55_XENTR PRELIMINARY;      PRT;   661 AA.
AC   Q6DF55;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   MGC88956 protein.
GN   Name=MGC88956;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC076888; AAH76888.1; -; mRNA.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR003885; LRR_Cyst.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00008; EGF; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00560; LRR_1; 8.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00365; LRR_SD22; 4.
DR   SMART; SM00369; LRR_TYP; 6.
DR   PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50026; EGF_3; 1.
SQ   SEQUENCE   661 AA;  71957 MW;  A0AC47946BE8DBEA CRC64;

Query Match             38.7%;  Score 1213.5;  DB 2;  Length 661;
Best Local Similarity   41.3%;  Pred. No. 2.6e-60;
Matches   282;  Conservative  88;  Mismatches 158;  Indels 155;  Gaps  20;

Qy    8  LLPLLLLLALGPGV--QGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT   65
         ||:|||||||:||   ..|||:||.||||:|||||||.|:||  ||||||||:||||||
Db    4  LLVWIILLATAQQMITEGCPAGCQCNTPQTVFCLARKNSNFPRSVPPDTLNLYVFENGIS   63

Qy   66  MLDASSFAGLPGLQLDLSQNQIASL--------------------------------  91
         :::|||| ||:||||||||||:||:
Db   64  SIEESSFIGLNGLHLLDLSHNQLSSLPGVFRNLANLSNLDLTSNQLTEISADTFQGLSR  123

Qy   92  ------------------------------------------RLPRLLLLDLSHNSLLALE  110
                                                    ::|||||||||:|||:|:
Db  124  LERLYLNGNRIRSIHPEAFKGIRSLLELKLSNNQLVTPPAFSLPHLLLLDLSYNAIPVLQ  183

Qy  111  PGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPVIRGLRGLTRLR   170
         |||.|.|.:||||||||||| |:||.||||||||||||:|||:.:||.:  |||||:|||
Db  184  QGVFNAGNIESLRLAGLGLKEVPEELLSGLKNLHELDLSDNQLDKVPP---GLHGLTKLN  240

Qy  171  LAGNTRIAQLRPDLAGLAGLAQLDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCP   230
         |||| :| |:||||.||.:|||||||.||||| |.||:|| ||||:::|||||||||:|
Db  241  IAGNVGFSQIQVDDLSNLPALQELDLSGLSLQTLPKGLTPKGLFRSSKRLRAVSLAQNPFNCVCS  300

Qy  231  LSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVV  290
         |.|:.||:| |.||||:|:|||||||||||||  | |.|:|:||.   ||:..:|||
Db  301  LGWLSEWMRVSGVVLLRPDETRCHFPPKNAGKTLRQLRDSEYGCPA-PTTIQMPSTMPP-  358

Qy  291  REPTALSSSLAPTWLSPTAP---ATEAPSPPSTAPPTVGPVPQPQD-----------CP  335
         |||| .|||||||   .:|:|      :.|:|:||||
Db  359  ------STTTGP----PTTTKHLQTEAPTTASTTTTIPHQEQEEDTQPFQFDFEDTLCP  408

Qy  336  PSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSL--TLG  392
         |.:||||||:|| | :||:|||||||:|||||:|  |  |  |   |.| :   | :|
Db  409  PQTCLNGGSCHLDPTGQLECECPPGFQGTYCET---------GPVTPAVVTEMYIEQVK  458

Qy  393  IEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRP  452
         |.|.:.|||||.||.|.|  |.:|:|:|||.||| .|.:|:.:  ||| ||||.|||:|:
Db  459  IEVTVSSIRVDLQSYSQNKE-KLRAIRLTVRNLYGADRRPMIYKLPPTLPEYTVRALSS  517

Qy  453  NATYSVCVMPLGPGRVPEGEEACGEAHT---PPAVHSNHAP-VTQAREGNLPLLIAPALA  508
         ||: |:|| .||  |   ||:.| |:|:     ||.|:|:| ||| :|||| |::.|.:|
Db  518  NSSYWVCLGSQGEGG-PB-EDLCTETHTLGEPP---KHSPQVTQSQEGNLTLVLVPAVA  571

Qy  509  AVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGE  568
         |.|| |:|::|   |.||:  |   : .|.     |          :||||.|||:||.
Db  572  AGILLS-AAVAAAACYARRR------KGKGHSVEDGGPLEMDGVK-----------KGLDGKGE  617

Qy  569  AL---------PSGSECEVPLM  581
         |          ::|:|||||||
Db  618  VKKLSEDPTGPEKTGAESEEPLM  640
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RESULT 9
Q503G2_BRARE
ID   Q503G2_BRARE PRELIMINARY;      PRT;   643 AA.
AC   Q503G2;
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DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein zgc:110624.
GN   Name=zgc:110624;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Singapore local strain; TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan M., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Singapore local strain; TISSUE=Embryo;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC095341; AAH95341.1; -; mRNA.
KW   Hypothetical protein.
SQ   SEQUENCE   643 AA;  70200 MW;  964B87924A7C642 CRC64;
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Query Match   29.6%;
Best Local Similarity   41.0%;
Matches 218;   Conservative   75;   Mismatches 198;   Indels   41;   Gaps   14;

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Qy     57 LYVFENGITMLDASSFAGLPGLQLLDLSQNQIA---SLRLPRLLLLDLSHSLLALEPGI 113
          |||::|||||:|:|:|||  :|:: ||||||::   :||:||||||::||||||:||:|
Db     84 LYLYSNIIQNIHPAAFBGLENLLELKLQGNQISVLPALQLPRLLLHLDLSYNSIPPLVAQD 143

Qy    114 LDTANVEALRLAGLGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLTRLRLAG 173
          |:: | :||: |:|  :|||||:: ||||| :|||||:|:| |::| |:|  |||:|||
Db    144 LQTPHLESLKIAGLGLTSLDEELLGSLINLHVLDVSQNQLVDVSONQLVDIQPTLKSMGGLRNLNLTG 203

Qy    174 NTRIAQLRPEDLAGLAALQELDVSNLLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSW 233
          | ::|: :|:||||| || |||||||:|||||||:|||||||||:|||||||||||| |:|
Db    204 NP-LGSLKHEDFQNLVNLLELDLSNLNLQGFPEGFNLFPKLEKLTAAENPFNCLCPLAW 262

Qy    234 FGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCGPATTTTATVPTTRPVVREP 293
          |||||||||||||||| :||||||:| |||||||:|||||||||:||:|||:|:| ::
Db    263 FPAWLKDVRVELLRTETRCHFPPINSGKVLEKLEHKDFGCPTTTIELTSAGTSSTTSKP 322

Qy    294 TALSSSLAPTWLSPTAPATEAPSPPSTAPP----TVGPVQPQD----CPPSTCLNG 342
          || ||  ||: |||| || |||||||||:||    :|:| :|:     ||:||:|||
Db    323 TNSSTQSGTTHIVPPAPLSDISSADADNFPVYQTTAFPSRIMEDSEGEGIMCPPNICLNG 382

Qy    343 GTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTP------VTPRPPRSLTLGIEP 395
          ||||| || |||||| :|  | :| | : |  | :||:      :|:| |||| | :||
Db    383 GTCIFKSNGVIVCLCCPPSMSGLYCEIQ-NEAMLPPPSPRVSLETIATVQPN---TISSHH 438

Qy    396 VSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNAT 455
          :: :|  | |||:|||  ::::|:  | || :||||:||||||||:|||:|:|||:||||
Db    439 ITSTSISLDLHRYIQ-TRPHIRGIRLTYSNLSGPDRRPLQLSVPPSYPEYTLRGLQPNST 497
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Qy    456 YSVCVMPLGPGRVPEGERACGEAHT---PPAVHSNHAPVTQAREGNLPLLIAPALAAVLL 512
          |||| ::| || |||: | |  | |   ||||:| ||| ::| :||||::|||| | |:|
Db    498 YSVCASPLGE-PVHASVSACMEARTAGIPPSSHEPSVDRTEPSSSLTPIVV--AVAVVMV 554

Qy    513 AALAAVGAAYCVRRGRAMAAAAQDKGVQGVPGAGPLELEGVKVPLEPG---PK 561
          || || || ||  :|    |:|  :| : | |: |:|  |||:| | |   ||
Db    555 VAIIAT-VVVISRRRPKAPVDMDLHE----TSPLEMEGVKTNPENGLTHPK 601
```

RESULT 10
Q4SQ68_TETNG

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ID   Q4SQ68_TETNG PRELIMINARY;       PRT;    962 AA.
AC   Q4SQ68;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 19 SCAF14535, whole genome shotgun sequence.
GN   ORFNames=GSTENG00014497001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetraodontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Catolico L., Poulain J., De Berardinis V.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014535; CAF97214.1; -; Genomic_DNA.
SQ   SEQUENCE   962 AA;  106856 MW;  3EC2C9402A2C80BF6 CRC64;
```

Query Match   29.2%;
Best Local Similarity   38.0%;   Score 914.5;   DB 2;   Length 962;
Matches 222;   Conservative   77;   Mismatches 190;   Indels   95;   Gaps   18;

```
Qy     57 LYVFENGITMLDASSFAGLPGLQLLDLSQNQIA--SLRLPRLLLLDLSHSLLALEPGI 113
          |||::|||||:|:|:|||  :|:: |||||::|:  :||:||||||::||||||:||:|
Db    388 LYLHGNLIQSIHAEAFBGLEMLLELKLQGNQLSSLPSLRFPRLLLLDLSNNNIPSLGPSD 447

Qy    114 LDTANVEALRLAGLGLQLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIR--GLRGLTRLRL 171
          |:: | :||: |:|   |||:: ||||||:||||:| ||:||:|::|| |  || |:||:|
Db    448 FQTPHLEALKIVSLGLMSLGDELIASMRNLHELDISMNQLTEVPLALKQDSLKGLIKLSL 507

Qy    172 AGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPL 231
          |||  :|::| :|||||| || |||||::|||||||:||||||||:||||||||||| |||
Db    508 AGNP-LGDLRVEDFEKLTSLQELDLSGLNLQGFSPSFLEMFPRLTQLTAAENPFNCLCPL 566

Qy    232 SWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVR 291
          ||  ||||||||||||| :|||||||:| |||||||:||||||||:||||||||:|:|:|:
Db    567 AWFPVWLKEKKVNLRRPEETRCHFPLVNAGKKLSALETRDFGCPLTT---TLP----IG 618
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Qy   61  ENGITMLDASSFAGLPGLQLLDSQNQIASLRL------PRLLLDLSHNSLLALEPG-I  113
            :|::.|:   .|.|.|  | :.|:   :.:|     ||||.:|:::||||
Db   59  DNNIARLEPGALAPLAALRRLYLHNNSLRALEAGAFRAQPRLLELALTSNRLRGLRSGAF  118

Qy  114  LDTANVEALRLAGLGLGQOLDEGLFSRLRNLHDLVSDNQLERVPPVIRGLRGLTRLRLAG  173
            :.|:  .|.|||||| | | ::.|.|:::|.||||:.:.|::.:
Db  119  VGLAQLRVLYLAGNQLARLLDFTFLHLPRLQELHLQENSIE------                159

Qy  174  NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSW  233
            :   :|| |:|||:||.|| |:.|||:|.:||.:::||  .|:|| ::||||.|.|.|.|
Db  160  ----LLEDQALAGLSSLALLDLSRNQLGTISREALQPLASLQVLRLTENPWRCDCALHW  214

Qy  234  FGPWVRESHVTLASPEETR--CHPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVR  291
            .|.|::|.  .|:|.:.:|  | .||  ||| |:|:|
Db  215  LGAWIKEGQRLLTSRDRKIMCAEPPRLALQSLLDVSHSSLIC------IPPSVHV--  264

Qy  292  EPTALSSSLAPTWLSPTAPATEAPSPPSTAPTTVGPVPVPQPDQDCPP--STCLNGGTCHLGT  349
            :| .|. :|.:|  |.|.:.   ::| .. :|: .|  : |  : :|  .| | .| .|
Db  265  QPLELTANLGED-LRVACQASGYPQP----LVTWRKVPQPREGRPRAQALEGL--LGL  317

Qy  350  RHHLACLCPEGF------------TGLY-CESQMQGG--------TRPSP-TPVTPRP  385
            |   .|:|  .|            ||.| ||.:. |
Db  318  GGHSASDTGSGMLFLSNITLAHAGKYECEASNAGGAARVPFRLLVNASRQQPQQPAQPPP  377

Qy  386  PRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLABY  445
            | .| |. |.|
Db  378  PAARPAGSEP---------                                           387

Qy  446  TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAP  505
            .: :|. .||:  .    :   |  | |::   ::     .|.|.     |||.:.|:. :
Db  388  ----------RPEAG-SMAFRALG------VATQ?---AIAA                     409

Qy  506  ALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGA--------GP--LELEGVK-  553
            |:| |  | :.:||.  .::| |:|:  |:  .  ||.|        .|  |.|.. :.
Db  410  AIALLALTALLLV-AMICRRRRRRKKA----RGPPGEGALFVNDYLDGPCTFAQLEELRD  464

Qy  554  ------VPLEPGPKATEGGGEALPSGSBCEVPLMGPFPGPGLQSP                 591
                  ||| |.||.:||::   |  |. |..|:. | |.|.
Db  465  ERGHEMFVINRSKPLFAEGPAEA---PADCG-PAQG-AGPGLRVP                 504
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Qy  292  EPTALSSSLAPTWLSPTAPATEAPSPPSTAP-----PTVGPVPVPQPD------------  333
            :| .|. :|.:|  |.|.:.:|.|: || :.|     ||:|.:: |
Db  619  SPTGSTSPIPVSTTPPRKMTYTNAIPPPPPPSEEILPSKTPYPLPPEPTFSPSSTGEVE  678

Qy  334  ---CPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGGQGTRPSPTPVTPRPPR--  387
               .||. | |||||| | |::.||:|| ..:|.|||.|:  |||
Db  679  SHICPANICLNGGTCHFDPMGQLSCICLSGTSGLYCEN--------VDIVPDPPKGHPV  728

Qy  388  ---SLTLGIEP----------VSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV  434
               ::.|.:.           |:.|: ::|::|:|: |.: | :| |:|||||||:| :|
Db  729  TEATLAASSVPVQNDAISSRQVTSTSILLDLQRFIE-TRPHIRGIRLIYRNLSGPDRRPM  787

Qy  435  TLRLPASLAEYTVTQLRPNATYSVCVMPLGP-------GRVPEGEEACGEAHT-------  480
            .|.:|||: ||:| .|:||.||||||.:||||       |.|| |:::|.:.
Db  788  ILSVPASYPEYTLRGLKPNCTYSVCASPLGERVSLRANSSVDTG--SCTEARTEGILMTS  845

Qy  481  PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV  540
            |.|. :.. .:|: .||:|.||:|:::| |.| ||.:| ||.|:||:.|::||
Db  846  SSATAPTPGPMT-----FTLLIAVSALALVLGVSLVAGTVTICVRK-RREAKAGMELEMA  898

Qy  541  GPGAGPLELEGVKVPLEPGPKATEGGGEALPSG----SECEVPL                 580
            ..||.|:|| ..:.| :.| ||||::||.|..|    |.|.|:|
Db  899  PADSDPMELDGMKLGLENGANGT------LPHKQAQINRCHTPL                 936
```

```
RESULT 11
Q50LG9_HUMAN
ID   Q50LG9_HUMAN   PRELIMINARY;        PRT;   513 AA.
AC   Q50LG9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LRRC24 protein.
GN   Name=LRRC24;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Shimizu N., Asakawa S., Shimizu A., Yamazaki S., Ishikawa S.K.;
RT   "Novel gene containing Leucine rich repeat on human chromosome 8.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB178281; BAD97811.1; -; mRNA.
DR   InterPro; IPR003599; Ig-like.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR011611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00560; LRR_1; 5.
DR   Pfam; PF01463; LRRCT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00369; LRR_TYP; 6.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Leucine-rich repeat; Repeat.
SQ   SEQUENCE   513 AA;  55199 MW;  3770FA80D979C1DE CRC64;

Query Match             11.8%;  Score 368.5;  DB 2;  Length 513;
Best Local Similarity   26.4%;
Matches  170;  Conservative   63;  Mismatches 217;  Indels 195;  Gaps  28;

Qy    1  MCSRVPLLPLLLLLALGPGVQGVQGSPSGCQCSGCQCSPQTVFCTARQSTTVPRDVPPDTVGLYVF  60
            |.||| ||||||||| ||.|   |.:: ||.| | |.| ::.|:|.:: ..:.||::|||||:
Db    1  MALRAPALLPLLLLL-LPLRAAGCPAACRC-YSATVECGALRLRVVPLGIPGTQTLPLQ  58
```

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RESULT 12
LRFN4_HUMAN
ID   LRFN4_HUMAN    STANDARD;           PRT;   635 AA.
AC   Q6PJG9; Q9BW70;
DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Leucine-rich repeat and fibronectin type-III domain containing protein
DE   4 precursor.
GN   Name=LRFN4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Eye, and Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Moore T., Max S., Wang J., Hsieh F.,
RA   Hopkins R.F., Jordan H., Moore T., Max S., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
```

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Qy    65  TMLDASSPAGLPGLQLLDLSQNQIASL------RLPRILLLDLSHNSLLALEPGIL-DTA  117
              |:  | : | |:  : |  : :             :|:
Db    61  QALGPPDFRNMTGLVDLTLSRNAITRIGARAFGDLESLRSLHLDGNRLVELGTGSLRGPV  120

Qy   118  NVEALRLAGLGLGQQLDEGLFSR-LRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNT  175
              ||:|| |  | | :||  :|    | | |  |:|:| ||    |    | |  | |
Db   121  NLQHLILSGNQLGRIAPGAFDDFLESLEDLDLSYNNLRQVPWAGIGAMPALHTLNLDHNL  180

Qy   176  RIAQLRPEDLAGLAALQBLDVSNLSLQALPGDLSGLFPRLR-------LLAAARNPFN  225
              : ||  ||  : | |  |||||||| |:|||  | ||  |          |  :|: | |
Db   181  -IDALPPGAFAQLGQLSRLDLTSNRLATLAPD--PLFSRGRDAEASPAPLVLSFSGNPLH  237

Qy   227  CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT  285
              : | |  |   | :| | | : :|        |:  | |  | | :| | |:  | :
Db   238  CNCELLWLR------RLARPDDLETCASPPGLAGRYFWAVPEGEFSC----------  278

Qy   286  TRPVVREPTALSSSLAPTWLSPTAPAT--EAPSPPSTAPPTVGPVPQ-----PQDCPP  336
                                                                :
Db   279  ------EPPLIARHTQRLWVLEGQRATLRCRALGDPAPTMHWVGPDDRLVGNSSRARAFP  332

Qy   337  STCLNGGTCHLGTRHHLACLC--PEGFTGLYCB--------SQMGQGTRPSPTPVTPR  384
              : |  |   | |   |: ||  :        :          |    |   |   | |
Db   333  NGTLEIGVTGAGDAGGYTCIATNPAGEATARVELRVLALPHGGNSSAEGGRPGPSDIAAS  392

Qy   385  PPRSL---TLGIEP--VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKRLVTL  436
              |  :|     | |     ||| | |: |: | |:    |     | |: |||  : | |
Db   393  ARTAAEGGTLESEPAVQVTEVTATSGLVSWGPRPADPVWMFQIQYN--SSEDETLIYR  450

Qy   437  RLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEA------CGEAHTPPAVHSNHAPV  491
              | ||:|  | |:||| | | |  :| |||||:| |||       || |   |  :|   |
Db   451  IVPASSHHFLLKHLVPGADYDLCLLALSPAAGPSDLTATRLLGCAHFSTLPASPLCHALQ  510

Qy   492  TQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPLELEG  551
              | | || | |||  ||  :| |:  |: |   ||| |
Db   511  AHVLGGTLTV---AVGGVLVAALLVFTVALLV-RGRG----------AGNGRLPLKLSH  555

Qy   552  VKVPLEPGPKAT  563
              | | |  |  | |
Db   556  VQSQTNGGPSPT  567
```

RESULT 13

RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimmond S., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.

```
DR   EMBL; BC000207; AAH00207.2; -; mRNA.
DR   EMBL; BC015581; AAH15581.2; -; mRNA.
DR   Ensembl; ENSG00000173621; Homo sapiens.
DR   HGNC; HGNC:28456; LRFN4.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 6.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00369; LRR_TYP; 6.
DR   SMART; SM00082; LRRCT; 1.
DR   PROSITE; PS50853; FN3; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat;
KW   Signal; Transmembrane.
FT   SIGNAL        1     16
FT   CHAIN        17    635       Leucine-rich repeat and fibronectin type-
FT                                III domain containing protein 4.
FT   TOPO_DOM     17    518       Extracellular (Potential).
FT   TRANSMEM    519    539       Potential.
FT   TOPO_DOM    540    635       Cytoplasmic (Potential).
FT   REPEAT       46     70       LRR 1.
FT   REPEAT       71     94       LRR 2.
FT   REPEAT       95    118       LRR 3.
FT   REPEAT      120    142       LRR 4.
FT   REPEAT      144    167       LRR 5.
FT   REPEAT      168    191       LRR 6.
FT   REPEAT      193    216       LRR 7.
FT   DOMAIN      281    367       Ig-like.
FT   DOMAIN      407    492       Fibronectin type-III.
FT   CARBOHYD     25     25       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     70     70       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    324    324       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    333    333       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    376    376       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    440    440       N-linked (GlcNAc...) (Potential).
FT   DISULFID    302    351       By similarity.
SQ   SEQUENCE   635 AA;  66860 MW;  13E6664SA17A92EE CRC64;
```

Query Match   11.5%; Score 359.5; DB 1; Length 635;
Best Local Similarity   27.6%; Pred. No. 3.4e-12;
Matches 169; Conservative 61; Mismatches 281; Indels 101; Gaps 23;

```
Qy     8  LLPLLLLLALGPGVQGCPSGCQC---SQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGI  64
              : |||||||||ASGAAACPLPCVCQNLSESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI
Db     1  MAPPLLLLLASGAAACPLPCVCQNLSESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI  60
```

```
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Eye, and Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
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DR   EMBL; AK081560; BAC38259.1; -; mRNA.
DR   EMBL; BC023036; AAH23036.1; -; mRNA.
DR   EMBL; BC023156; AAH23156.1; -; mRNA.
DR   HSSP; Q9B2R6; 1P8T.
DR   Ensembl; ENSMUSG00000045045; Mus musculus.
DR   MGI; MGI:2385612; Lrfn4.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 6.
DR   PRINTS; PR00019; LEURICHRPT.
DR   PROSITE; PS50853; FN3; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat;
KW   Signal; Transmembrane.
FT   SIGNAL        1     16       Potential.
FT   CHAIN        17    636       Leucine-rich repeat and fibronectin type-
FT                                III domain containing protein 4.
FT   TOPO_DOM     17    518       Extracellular (Potential).
FT   TRANSMEM    519    539       Potential.
FT   TOPO_DOM    540    636       Cytoplasmic (Potential).
FT   REPEAT       46     70       LRR 1.
FT   REPEAT       71     94       LRR 2.
FT   REPEAT       95    118       LRR 3.
FT   REPEAT      120    142       LRR 4.
FT   REPEAT      144    167       LRR 5.
FT   REPEAT      168    191       LRR 6.
FT   REPEAT      193    216       LRR 7.
FT   DOMAIN      281    367       Ig-like.
FT   DOMAIN      407    492       Fibronectin type-III.
FT   CARBOHYD     25     25       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     70     70       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    324    324       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    333    333       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    376    376       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    440    440       N-linked (GlcNAc...) (Potential).
FT   DISULFID    302    351       By similarity.
FT   CONFLICT    503    503       T -> N (in Ref. 2; AAH23156).
SQ   SEQUENCE   636 AA;  67252 MW;  1EE86896CB88BA91 CRC64;

Query Match             11.2%;  Score 351;  DB 1;  Length 636;
Best Local Similarity   27.2%;  Pred. No. 1e:11;
Matches  170;  Conservative   62;  Mismatches  276;  Indels  116;  Gaps  25;

Qy         8 LLPLLLLLLALGPGVQGCPSGCQC--SQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGI 64
             : ||||||||: |||  ||| | |    |: ||  | || |:   | |: |||||:.: :|
Db         1 MAPPLLLLLLASGAAACPLPCVCQNLSESLSTLCAHRGLLFVPPNVDRRTVELRLADNFI 60

Qy        65 TMLDASSFAGLPGLQLDLSQNQIASL------RLPRLLLDLSHNSLLAL-EPGILDTA 117
             : |  :.| ||| |: |||.||| :       ||.||||:||:| |  :  .|: |.
Db        61 QALGPPDFRNMTGLVDLTLSRNAITRIGARSFGDLESLRSLHLDGNRLVELGSSSLRGPV 120

Qy       118 NVEALRLAGLGLQQLDEGLFSR-LRNLHDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNT 175
             |:: | |:| .|  :  |:|.   ::|| |||| |:| .:| |. .|  . :  |.|.:|
Db       121 NLQHLILSGNQLGRIAPGAFDDFLDSLEDLDVSYNNRLRQVPWAGIGSMPALHTLNLDHNL 180

Qy       176 RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLR-----LLAAARNPFN 226
              | :|   :: .: |:|.|||| |:|  :  |  .|||.     : : :  ..| | 
Db       181 -IDALPPGVFAQLSQLSRIDLTSNRLATLIAPD--PLFSRGRDAEASPSPLVLSFSGNPLH 237

Qy       227 CVCPLSWFGPWVRESHVTLASPEETR-CHFPPKNAGRLLLELDYADFGCPATTTTATVPT 285
              | |  ||   ||                  .  | |  |   : :   |::  : :
Db       238 CNCELLWLR------RLARPDDLETCASPPTLAGRYFWAVPEGEFSC------ 278

Qy       286 TRPVVREPTALSSSLAPTWLSPTAPAT--EAPSPPSTAPPTVGPVPQQD 333
              .|   ||   |   | | ||.  . |      .   :|    | |:   :
Db       279 ------EPPLIARHTQRLWVLEGQRATLRCRALGDPVPTMHWVG---PDDRLVGNSSRA 328

Qy       334 -CPPSTCLNGGTCHLGTRHHLACLC--PEGFTGLYCESQM--------GQGTRPSPTP 380
                  .|.  | |:  |: .    |    |.   .   .::        | |.| . .
Db       329 WAFPNGTLEIGVTGAGDAGAYTCIATNPAGEATARVELRVLALPHGGNTSAEGGRPGPSD 388

Qy       381 VTPRPPRSL----TLGIEP---VSPTSLRVGLQRYLQGSSVQ-LRSLRLTYRNLSGPDKR 432
             |:   | |    :| .:     |:|. | | |.|::    :|  | | | : : ||
Db       389 IAASARTAEGEGTLESEPAVQVTEVTATSGLVSWGLGRPADPVWMFQIYN--SSEDET 446

Qy       433 LVTLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEA----CGEAHTPPAVHSN 487
             |: : :|:| .  :     | | | : |:   | | :  .       | :| : |.
Db       447 LIYRIVPASSHHFLLKHLVPGADYDLCLLALSPAAGPSDLTATRLLGCAHFSTLPATPLC 506

Qy       488 HAPVTQAREGNLPLLIAPALAAVLLAALAAAVGAAYCVRRGRAMAAAAQDKGQVGPGAGPL 547
             ||    : || | |: | |  |:| ||  .  | : || | .
Db       507 HALQAHVLGGTLTV---AVGGVLVAALLVFTVALLV-RGRG------AGNGRLPL 551

Qy       548 ELEGVKVPLEPGPKATEGGGEALP 571
              :| |:.       .|.| ||. .
Db       552 KLSHVQ------SQTNGGTSPMP 568
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RESULT 14
Q8BLU0_MOUSE
ID   Q8BLU0_MOUSE    PRELIMINARY;     PRT;   660 AA.
AC   Q8BLU0;
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DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE   enriched library, clone:A530098L04 product:KIAA0405 (LEUCINE-RICH
DE   REPEAT TRANSMEMBRANE PROTEIN FLRT2) homolog (Fibronectin leucine rich
DE   transmembrane protein 2).
GN   Name=Map4k5; Synonyms=Flrt2;
OS   Mus musculus (Mouse)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format

RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda T., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6xCBA;
RA   Haines B.P., Summerbell D., Rigby P.W.J.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N;
RC   TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC   virgin mouse. Taken by biopsy.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N;
RC   TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC   virgin mouse. Taken by biopsy.;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK041311; BAC30900.1; -; mRNA.
DR   EMBL; AY495669; AAR92202.1; -; mRNA.
DR   EMBL; BC096471; AAH96471.1; -; mRNA.
DR   HSSP; P07359; 1M0Z.
DR   Ensembl; ENSMUSG00000047414; Mus musculus.
RG   MGI; MGI:1925503; Map4k5.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   InterPro; IPR001211; PhospholipaseA2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00560; LRR_1; 8.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
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DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00369; LRR_TYP; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
DR   PROSITE; PS50053; FN3; 1.
KW   Leucine-rich repeat; Repeat; Transmembrane.
SQ   SEQUENCE  660 AA;  73948 MW;  5C1A9BBA3142C020 CRC64;

Query Match             10.9%;     Score 341;   DB 2;   Length 660;
Best Local Similarity   23.1%;     Pred. No. 3.9e-11;
Matches   143;  Conservative   85;  Mismatches  238;  Indels  154;  Gaps  19;

Qy     4 RVPLLLPLLLLALGPGVQ-----GCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLY  58
           :|| :||||| |:: ||
Db    11 RGAFILKFWLIISLGLYLQVSKLLACPSVCRCDR-NFVYCNERSLTSVPLGIPEGVTVLY  69

Qy    59 VF-------------------------------------ENGITMLDASSF  72
          :|
Db    70 LHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTISRAAL 129

Qy    73 AGLPGLQLLDLSQNQIASLRLP--------RLLLLDLSHNSLLALEPGI---LDTANVEA 121
          |:|| ||||| :|| |        :|: |||::|| |||  :
Db   130 AQLLKLEELHLDDNSISSTVGVEDGAFREAISLKLLFLLSKNHLSSVPVGLPVDLQELRVDE 189

Qy   122 LRLA---GLGLQQLD-----------------EGLFSRLRNLHDLDVSDNQLERVPPVI 160
          :|||             : ||
Db   190 NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDL 249

Qy   161 RGLRGLTRLRLAGNTRIAQLRPEDLAGLAAALQELDVSNLSLQALPGDLSGLFPRLRILAA 220
          || :|:|| :|  | :|||
Db   250 PGTH-LIRLYLQDN-QINHIPLTAFANLRKLERLDISNNQLRMLTQGVFDHLSNLKQLTA 307

Qy   221 ARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTT 280
          |||     ::|: |  :|   ||
Db   308 RNNPWFCDCSIKWVTEWLKYIPSSL-NVRGFMCQGPEQVRGMAVRELNMNLLSCPTTTPG 366

Qy   281 ATVPTTRPVVREPTALSSSLAPTWLSPTTAPATEAPSPPSTAPPTVGPVPQPDCPPSTCL 340
          |  :|||
Db   367 LPVFTPAP-----------------STVSPTTQSPTL------SVPSPSRGSVPPAPTPSKLPFTIPDW 411

Qy   341 NGGTCHLGTRHHLACLCPEGFTGLYCESSQMGGQTRPSPTPVTPRPPRSLTLGIEPVSPTS 400
          |:
Db   412 DG----------------------------------RERVTPPISERIQLSIHFVNDTS 436

Qy   401 LRVGLQRYLQGGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY-TVTQLRPNATYSVC 459
          ::|       :: :  ||:  :||  ::|:
Db   437 IQVSWLSLFTVMAYKLTWVKMGHSLVGG----IVQERIVSGEKQHLSLVNLEPRSTYRIC 492

Qy   460 VMPLGPGRVPEGEEA-CGEAHTPPA-------VHSNHAPVTQAREGNLPLLIAPALAAVL 511
          :||||                          :|||
Db   493 LVPLDAFNYRTVEDTICSEATTHASYLNNGSNTASSHQTTSHSMGS-PFFLAGLIGGAV 551

Qy   512 LAALAAVGAAYC---VRRGR 528
          : ||
Db   552 IFVLVLLSVFCWHMHKKGR 571

RESULT 15
Q8BHA1_MOUSE
ID   Q8BHA1_MOUSE  PRELIMINARY;    PRT;    521 AA.
AC   Q8BHA1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE   library, clone:C230002N12 product:hypothetical Zinc carboxypeptidases,
DE   carboxypeptidase A metalloprotease (M14) family containing protein,
DE   full insert sequence (Mus musculus adult male olfactory brain cDNA,
DE   RIKEN full-length enriched library, clone:6430402H13
DE   product:hypothetical Zinc carboxypeptidases, carboxypeptidase A
DE   metalloprotease (M14) family containing protein, full insert
DE   sequence).
GN   Name=Lrrc14;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang N.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
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Query Match   10.8%; Score 339; DB 2; Length 521;
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Matches 149; Conservative 66; Mismatches 217; Indels 120; Gaps 21;

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Qy    1 MCSRVPLLPL---LLLLALGPGV----QGCPSGCQCSQPQTVFCTARQGTTVPRDVPPD 53
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Db    1 MALRAPTLLLLGLLLLLPLLPLLPGLPPRATGCPAACRC-YSATVECGALRLRVVPPGIPPG 59

Qy   54 TVGLYVFENGITMLDASSFAGLPGLQLLDLSQNOIASLR------LPRLLLLDLSHNSLL 107
          | :| | : :| | | ::  :| :|  ||||| :  ||       |||| | ||||||
Db   60 TQTLFLQDNSIAHLEQGSLAPLAALRHLYLHNNTLRALESGAFRAQPRLLELALTGNRLR 119

Qy  108 ALEPG-ILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVVIRGLRGL 166
          :| :| | | : :| :|||  :| |    : : :  :|   ::|::
Db  120 GLRGGAFVGLVQLRVLYLAGNQLAKLLDFTFLHLPRLQELHLQENSIE----------- 167

Qy  167 TRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFN 226
          : |||   :  | || |:|   :| | |   ::| |     |  :  |
Db  168 ------------LLEDQALAGLSSLALLDLSRNQLGTISKEALQPLSSLQVLRLTENPWR 215

Qy  227 CVCPLSWFGPWVRESHVTLASPEETR--CHPPPKNAGRLLLELDYADFGCPATTTTATVP 284
          | |:|:| | : |      :::  | :  | |||   |     :  | |  ::|
Db  216 CDCALHWLGSWIKEGGRRLLSSRDKKITCAEPPRLALQSLLEVSGGSLIC--------IP 267

Qy  285 TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPP--STCLNG 342
          :   :   || | : |  |      |  | |  ::        | |||      | | |
Db  268 PSVNV--EPPEFTANLGED-LQVACQASGYPQP----LVVWRKVPQPRDGKPQAQAQLEG 320

Qy  343 GTCHLG--------------TRHHLACLCPEGFTGLY-CESQMGQGTRPSPTPVTPRPPR 387
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Db  321 GAPGLGHGTRDTGSGMLFLTNITLA------HAGKYECEAANAGGKARVPFHLLVNASR 374

Qy  388 SLTLGI-EPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTL--------- 436
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Db  375 QQSQQLPDPQAPATRPVGHEPQHEAGSMAFRALGLATQTAITAAIALLALTALLLAAMIC 434

Qy  437 ------RLPASLAEYT-------------VTQLRPNATYSVCVM----PLGPGRVPE 470
              | |:::| :|              ::| |:    | |     |||| |||
Db  435 RRRRRRKKVPAPSGEGTLFVNDYSDGPCTFAQLEBLRDDHGHBMFVIDRSKPLFPEVLP- 493

Qy  471 GEEACGEAHTPP 482
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Db  494 -EEA--PEHNPP 502
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Job time : 271 secs

RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai K., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK048678; BAC33419.1; -; mRNA.
DR   EMBL; AK078176; BAC37163.1; -; mRNA.
DR   HSSP; Q9BZR6; 1OZN.
DR   Ensembl; ENSMUSG00000033707; Mus musculus.
DR   MGI; MGI:2445060; Lrrc14.
DR   GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00560; LRR_1; 4.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00369; LRR_TYP; 3.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Carboxypeptidase; Hypothetical protein; Immunoglobulin domain;
KW   Leucine-rich repeat; Metalloprotease; Protease; Repeat.
SQ   SEQUENCE 521 AA; 56334 MW; 3D1E4BEE30228A6 CRC64;

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GenCore version 5.1.6
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 243163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

No.   Score Match Length DB ID   Description

RESULT 1
ID AAY06484 standard; protein; 598 AA.
DE Human tumour-associated protein PRO357.
PN WO9935170-A2.
PD 15-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 2; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 2
ID AAB01322 standard; protein; 598 AA.
DE Human PRO357 polypeptide.
PN WO200032776-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 3; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 3
ID AAY93691 standard; protein; 598 AA.
DE Amino acid sequence of novel polypeptide PRO357.
PN WO200208288-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 3; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 4
ID AAU83643 standard; protein; 598 AA.
DE Human PRO protein, Seq ID No 104.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 5; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 5
ID ADY31844 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN WO200193983-A1.
PD 13-DEC-2001.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 5; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 6
ID ABU55931 standard; protein; 598 AA.

DE Human secreted/transmembrane protein PRO357.
PN US2002142959-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 7
ID ABU80790 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 8
ID ABO33756 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 9
ID ABU60241 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002132768-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 10
ID ABU64927 standard; protein; 598 AA.
DE Human secreted/transmembrane protein PRO357.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 11
ID ABU58361 standard; protein; 598 AA.
DE Novel human secreted protein PRO357.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 12
ID ABU57247 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 13
ID ABU56312 standard; protein; 598 AA.
DE Human secreted/transmembrane protein, PRO357.
PN US2002213981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 14
ID ABU60352 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match   100.0%;   Score 3135;   DB 6; Length 598;
Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 15
ID ABU82099 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.

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PN   US2003088063-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
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     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 16
ID   ABU11313 standard; protein; 598 AA.
DE   Human pro357 protein sequence.
PN   US2002127643-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 6;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 17
ID   ABU67132 standard; protein; 598 AA.
DE   Human PRO polypeptide #12.
PN   US2002165143-A1.
PD   07-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 6;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 18
ID   ABJ72279 standard; protein; 598 AA.
DE   Human PRO357 protein.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 6;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 19
ID   ABJ72407 standard; protein; 598 AA.
DE   Human PRO357 protein.
PN   US2003027988-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 6;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 20
ID   ABO34302 standard; protein; 598 AA.
DE   Human membrane bound receptor/protein PRO357 amino acid sequence.
PN   US2003044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 6;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 21
ID   ABJ72109 standard; protein; 598 AA.
DE   Human secreted/transmembrane polypeptide PRO 357.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 22
ID   ADB83594 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088068-A1
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 23
ID   ADB80700 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088068-A1
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 24
ID   ADB73241 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096968-A1.
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PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
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     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 25
ID   ADB78323 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 26
ID   ADB84971 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 27
ID   ADB78077 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 28
ID   ADB87143 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003088067-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 29
ID   ADB84725 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 30
ID   ADB83840 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 31
ID   ADB72995 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 32
ID   ADC25825 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2002142419-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135; DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 33
ID   ADC25583 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2002215004-A1.
PD   24-OCT-2002.
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PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 34
ID   ADC25704 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2003077698-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 35
ID   ADC36833 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 36
ID   ADC21823 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 37
ID   ADC49854 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 38
ID   ADC49053 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 39
ID   ADC49570 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 40
ID   ADC47431 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 41
ID   ADC47176 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 42
ID   ADC78051 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.

     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 43
ID   ADD06286 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003078816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 44
ID   ADC77805 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 45
ID   ADD50768 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 46
ID   ADD51014 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 47
ID   ADD50495 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 48
ID   ADD50249 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 49
ID   ADD51260 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 50
ID   ADH27489 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2003083479-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 7;   Length 598;
     Best Local Similarity  100.0%;   Pred. No. 3.8e-190;
RESULT 51
ID   ADC4807 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003092888-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            100.0%;   Score 3135;   DB 8;   Length 598;
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   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 52
ID   ADE20978 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 53
ID   ADE05822 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 54
ID   ADD75051 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 55
ID   ADD75797 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 56
ID   ADD85029 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 57
ID   ADD86855 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 58
ID   ADE20732 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 59
ID   ADE39029 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096362-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 60
ID   ADE05576 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;

RESULT 61
ID   ADD73561 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 62
ID   ADD78401 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 63
ID   ADE21224 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 64
ID   ADD77339 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 65
ID   ADE20486 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 66
ID   ADD75551 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 67
ID   ADD74067 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 68
ID   ADD74313 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 69
ID   ADD76043 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
   Query Match             100.0%;   Score 3135;   DB 8;   Length 598;
   Best Local Similarity   100.0%;   Pred. No. 3.8e-190;
RESULT 70
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ID  ADD85535 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100721-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 71
ID  ADE05084 standard; protein; 598 AA.
DE  Human PRO polypeptide #52.
PN  US2003100726-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 72
ID  ADD75297 standard; protein; 598 AA.
DE  Human PRO polypeptide #52.
PN  US2003100714-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 73
ID  ADD76841 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100715-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 74
ID  ADD86609 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100719-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 75
ID  ADD78077 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003096742-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 76
ID  ADE71538 standard; protein; 598 AA.
DE  Human secreted/transmembrane PRO polypeptide #12.
PN  US2003100731-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 77
ID  ADD77585 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100729-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 78
ID  ADD77831 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100730-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 79
ID  ADD85289 standard; protein; 598 AA.

DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100725-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 80
ID  ADD73821 standard; protein; 598 AA.
DE  Human PRO polypeptide #52.
PN  US2003100710-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 81
ID  ADD74559 standard; protein; 598 AA.
DE  Human PRO polypeptide #52.
PN  US2003100713-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 82
ID  ADD77087 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100716-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 83
ID  ADD85781 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003100720-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 84
ID  ADE05330 standard; protein; 598 AA.
DE  Human PRO polypeptide #52.
PN  US2003100723-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 85
ID  ADD74805 standard; protein; 598 AA.
DE  Human PRO polypeptide #52.
PN  US2003100724-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 86
ID  ADG05617 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
PN  US2003096959-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 87
ID  ADG27171 standard; protein; 598 AA.
DE  Human PRO polypeptide #52.
PN  US2003096962-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
    Best Local Similarity  100.0%;  Pred. No. 3.8e-190;
RESULT 88
ID  ADG11234 standard; protein; 598 AA.
DE  Novel human secreted and transmembrane protein PRO357.
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PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 89
ID   ADG12013 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 90
ID   ADF94570 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 91
ID   ADG06666 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003211570-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 92
ID   ADG63481 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 93
ID   ADH39010 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 94
ID   ADH43210 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2003207401-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 95
ID   ADG34100 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 96
ID   ADI33570 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2003096960-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 97
ID   ADH69664 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2004019183-A1.


PD   29-JAN-2004.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 98
ID   ADI29825 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2003096961-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 99
ID   ADM27222 standard; protein; 598 AA.
DE   Novel human secreted and transmembrane protein PRO357.
PN   US2004044179-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 100
ID   ADK66580 standard; protein; 598 AA.
DE   Human PRO polypeptide #52.
PN   US2004044180-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 101
ID   ADN00448 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2004091972-A1.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 102
ID   ADU25372 standard; protein; 598 AA.
DE   Human secreted/transmembrane PRO polypeptide #12.
PN   US2004220385-A1.
PD   04-NOV-2004.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 8;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 103
ID   ADY39535 standard; protein; 598 AA.
DE   Human insulin-like growth factor homolog PRO357 precursor protein.
PN   US2005048613-A1.
PD   03-MAR-2005.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 9;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 104
ID   ADY73816 standard; protein; 598 AA.
DE   Human PRO357 protein, SEQ ID NO: 69.
PN   US2005059115-A1.
PD   17-MAR-2005.
PA   (GETH ) GENENTECH INC.
     Query Match    100.0%;  Score 3135;  DB 9;  Length 598;
     Best Local Similarity 100.0%;  Pred. No. 3.8e-190;
RESULT 105
ID   AAY17831 standard; protein; 598 AA.
DE   Human PRO357 protein sequence.
PN   WO9928462-A2.
PD   10-JUN-1999.
PA   (GETH ) GENENTECH INC.
     Query Match    99.7%;  Score 3126;  DB 2;  Length 598;
     Best Local Similarity 99.8%;  Pred. No. 1.4e-189;
RESULT 106
ID   AAB07428 standard; protein; 673 AA.
DE   Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).
PN   WO200042170-A1.
PD   20-JUL-2000.
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PA    (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
      Query Match       98.4%;   Score 3083.5;   DB 3;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 107
ID    AAB87533 standard; protein; 673 AA.
DE    Human PRO1282.
PN    WO200116318-A2.
PD    08-MAR-2001.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 4;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 108
ID    AAB65166 standard; protein; 673 AA.
DE    Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.
PN    WO200073454-A1.
PD    07-DEC-2000.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 4;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 109
ID    AAU75266 standard; protein; 673 AA.
DE    Human Slit-like protein #1.
PN    WO200212346-A2.
PD    14-FEB-2002.
PA    (PHAA ) PHARMACIA CORP.
      Query Match       98.4%;   Score 3083.5;   DB 5;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 110
ID    ABG95858 standard; protein; 673 AA.
DE    Human secreted/transmembrane protein PRO1282.
PN    US2002119130-A1.
PD    29-AUG-2002.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 5;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 111
ID    ABG78042 standard; protein; 673 AA.
DE    Human leucine-rich surface glycoprotein (LRSG-1).
PN    US2002072089-A1.
PD    13-JUN-2002.
PA    (HOLT/) HOLTZMAN D A.
PA    (MCCA/) MCCARTHY S A.
PA    (MACB/) MACBETH K J.
PA    (BUSF/) BUSFIELD S J.
PA    (PANY/) PAN Y.
PA    (WHIT/) WHITE D.
PA    (KHOD/) KHODADOUST M M.
PA    (GUWW/) GU W.
      Query Match       98.4%;   Score 3083.5;   DB 5;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 112
ID    ABU57981 standard; protein; 673 AA.
DE    Human PRO polypeptide #13.
PN    US2003027163-A1.
PD    06-FEB-2003.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 113
ID    ABU59059 standard; protein; 673 AA.
DE    Novel human secreted or transmembrane protein PRO1282.
PN    US2002133252-A1.
PD    19-SEP-2002.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 114
ID    ABU82571 standard; protein; 673 AA.
DE    Human secreted/transmembrane protein PRO1282.
PN    US2003032023-A1.
PD    13-FEB-2003.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 115

ID    ABU60490 standard; protein; 673 AA.
DE    Human secreted/transmembrane protein, #19.
PN    US2002160384-A1.
PD    31-OCT-2002.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 116
ID    ABU13872 standard; protein; 673 AA.
DE    Human PRO1282 polypeptide.
PN    US2002103125-A1.
PD    01-AUG-2002.
PA    (GETH ) GENENTECH LTD.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 117
ID    ABU72457 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003003531-A1.
PD    02-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 118
ID    ABU90883 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003018173-A1.
PD    23-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 119
ID    ABO33942 standard; protein; 673 AA.
DE    Human secreted/transmembrane protein PRO1282.
PN    US2003009013-A1.
PD    09-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 120
ID    ABU71959 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003018183-A1.
PD    23-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 121
ID    ABU71513 standard; protein; 673 AA.
DE    Human secreted polypeptide PRO1282.
PN    US2003013855-A1.
PD    16-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 122
ID    ABU72294 standard; protein; 673 AA.
DE    Human PRO polypeptide #8.
PN    US2002182638-A1.
PD    05-DEC-2002.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 123
ID    ABU90967 standard; protein; 673 AA.
DE    Human PRO polypeptide #8.
PN    US2003018168-A1.
PD    23-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match       98.4%;   Score 3083.5;   DB 6;   Length 673;
      Best Local Similarity  88.7%;   Pred. No. 8.1e-187;
RESULT 124
ID    ABU59206 standard; protein; 673 AA.
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DE   Human secreted/transmembrane protein, #19.
PN   US2003027162-A1.
PD   06-FEB-2003.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 125
ID   ABO25903 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2002127576-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 126
ID   ABO27288 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO1282.
PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 127
ID   ABU92483 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 128
ID   ABU81153 standard; protein; 673 AA.
DE   Human secreted polypeptide PRO1282.
PN   US2003027712-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 129
ID   ABO53268 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003027986-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 130
ID   ABU58912 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein, #19.
PN   US2002142961-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 131
ID   ABU92290 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003022187-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 132
ID   ABU59355 standard; protein; 673 AA.
DE   Novel human secreted or transmembrane protein PRO1282.
PN   US2003027985-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 133
ID   ABU98270 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.

     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 134
ID   ABU89275 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 135
ID   ABU82482 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002183494-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 136
ID   ABU92121 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003017476-A1.
PD   23-JAN-2003.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 137
ID   ABU96446 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003027993-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 138
ID   ABU10827 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2002123463-A1.
PD   05-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 139
ID   ABU81579 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2002177164-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 140
ID   ABU72116 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003023042-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 141
ID   ABU88518 standard; protein; 673 AA.
DE   Human secreted and transmembrane polypeptide PRO1282.
PN   US2002197615-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 142
ID   ABO34032 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2003017981-A1.
PD   23-JAN-2003.
     Query Match              98.4%;   Score 3083.5;  DB 6;  Length 673;
     Best Local Similarity    88.7%;   Pred. No. 8.1e-187;
RESULT 143
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ID   ADB17073 standard; protein; 673 AA.
DE   Human transmembrane PRO polypeptide (SeqID 16).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 144
ID   ADA37563 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 145
ID   ADA21249 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO1282.
PN   US2003054404-A1.
PD   20-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 146
ID   ABO44246 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO 1282.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 147
ID   ADA10036 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein, PRO1282.
PN   US2003059831-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 148
ID   ADA19878 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 149
ID   ADB17261 standard; protein; 673 AA.
DE   Human transmembrane PRO polypeptide (SeqID 16).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 150
ID   ADA17580 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 151
ID   ADA27688 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003054459-A1.
PD   20-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 152
ID   ADA20050 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003055222-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 153
ID   ABO34174 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO 1282.
PN   US2003060601-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 154
ID   ADA94268 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282
PN   US2003059832-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 155
ID   ADA38493 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003059780-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 156
ID   ADA92614 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003060407-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 157
ID   ADA00347 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO 1282.
PN   US2003027992-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%; Score 3083.5; DB 6; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 158
ID   ABO53118 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003044806-A1.
PD   06-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 159
ID   ADA22175 standard; protein; 673 AA.
DE   Human secreted/transmembrane polypeptide PRO1282.
PN   US2003040473-A1.
PD   27-FEB-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 160
ID   ABO22488 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003017982-A1.
PD   23-JAN-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 161
ID   ADA06341 standard; protein; 673 AA.
DE   Human secreted/transmembrane PRO polypeptide #13.
PN   US2003049638-A1.
PD   13-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;
     Best Local Similarity 88.7%; Pred. No. 8.1e-187;

RESULT 162
ID   ADA39034 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003059782-A1.
PD   27-MAR-2003.
     Query Match   98.4%; Score 3083.5; DB 7; Length 673;

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Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 163
ID    ADB85589 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003049735-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 164
ID    ADB96060 standard; protein; 673 AA.
DE    Human PRO1282 polypeptide #13.
PN    US2003054403-A1.
PD    20-MAR-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 165
ID    ADB68268 standard; protein; 673 AA.
DE    Human PRO1282 protein.
PN    US2003065161-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 166
ID    ADB68075 standard; protein; 673 AA.
DE    Human PRO1282 protein.
PN    US2003060600-A1.
PD    27-MAR-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 167
ID    ADB90892 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003083473-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 168
ID    ADC57532 standard; protein; 673 AA.
DE    Human PRO1282 polypeptide #13.
PN    US2003027754-A1.
PD    06-FEB-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 169
ID    ADC54896 standard; protein; 673 AA.
DE    Human PRO1282 polypeptide #13.
PN    US2003045463-A1.
PD    06-MAR-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 170
ID    ADC11763 standard; protein; 673 AA.
DE    Human secreted/transmembrane protein PRO1282.
PN    US2003049681-A1.
PD    13-MAR-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 171
ID    ADC06972 standard; protein; 673 AA.
DE    Human PRO1282 protein.
PN    US2003060602-A1.
PD    27-MAR-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 172
ID    ADC56185 standard; protein; 673 AA.
DE    Human PRO1282 polypeptide #13.
PN    US2003064375-A1.
PD    03-APR-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 173
ID    ADC17151 standard; protein; 673 AA.
DE    Mammalian PRO polypeptide (SeqID 16).
PN    US2003065141-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 174
ID    ADC07240 standard; protein; 673 AA.
DE    Human secreted/transmembrane protein PRO1282.
PN    US2003068647-A1.
PD    10-APR-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 175
ID    ADC11230 standard; protein; 673 AA.
DE    Human secreted/transmembrane protein PRO1282.
PN    US2003069403-A1.
PD    10-APR-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 176
ID    ADC14849 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003073208-A1.
PD    17-APR-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 177
ID    ADC52344 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003313888-A1.
PD    24-JUL-2003.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 178
ID    ADC14352 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003082546-A1.
PD    01-MAY-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 179
ID    ADD07884 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003068623-A1.
PD    10-APR-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 180
ID    ADC81709 standard; protein; 673 AA.
DE    Human PRO polypeptide #13.
PN    US2003083461-A1.
PD    01-MAY-2003.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 181
ID    ADD07351 standard; protein; 673 AA.
DE    Novel human secreted and transmembrane protein PRO1282.
PN    US2003219299-A1.
PD    19-DEC-2002.
PA    (GETH ) GENENTECH INC.
Query Match             98.4%;    Score 3083.5; DB 7;   Length 673;
Best Local Similarity   88.7%;    Pred. No. 8.1e-187;
RESULT 182
ID    ADC82242 standard; protein; 673 AA.
DE    Human PRO polypeptide #13.
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PN  US2003059833-A1.
PD  27-MAR-2003.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 183
ID  ADD08422 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003073090-A1.
PD  17-APR-2003.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 184
ID  ADD06671 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2002193300-A1.
PD  19-DEC-2002.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 185
ID  ADC82918 standard; protein; 673 AA.
DE  Human PRO polypeptide #13.
PN  US2003059783-A1.
PD  27-MAR-2003.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 186
ID  ADD55025 standard; protein; 673 AA.
DE  Human PRO polypeptide #13.
PN  US2003077593-A1.
PD  24-APR-2003.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 187
ID  ADD36020 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003105298-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 188
ID  ADD55983 standard; protein; 673 AA.
DE  Human PRO polypeptide #13.
PN  US2003077594-A1.
PD  24-APR-2003.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 189
ID  ADD54421 standard; protein; 673 AA.
DE  Human PRO polypeptide #13.
PN  US2002132253-A1.
PD  19-SEP-2002.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 190
ID  ADE26575 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003087304-A1.
PD  08-MAY-2003.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 191
ID  ADE26042 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003087305-A1.
PD  08-MAY-2003.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 192
ID  ADF66979 standard; protein; 673 AA.
DE  Human PRO1282 amino acid sequence SEQ ID NO:52.

PN  US2002219148-A1.
PD  26-DEC-2002.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 193
ID  ADG01021 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003078387-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 194
ID  ADG08574 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180793-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 195
ID  ADF95195 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180795-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 196
ID  ADH24048 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180918-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 197
ID  ADH34074 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180858-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 198
ID  ADH29907 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180859-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 199
ID  ADH23878 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180919-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 200
ID  ADG85282 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180904-A1.
PD  25-SEP-2003
PA  (GETH ) GENENTECH INC.
    Query Match     98.4%;  Score 3083.5;  DB 7;  Length 673;
    Best Local Similarity  88.7%;  Pred. No. 8.1e-187;
RESULT 201
ID  ADH24558 standard; protein; 673 AA.
DE  Novel human secreted and transmembrane protein PRO1282.
PN  US2003180907-A1.
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PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 202
ID   ADH37414 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003181646-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 203
ID   ADH02003 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180837-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 204
ID   ADH37584 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003181648-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 205
ID   ADG85622 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180905-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 206
ID   ADH24218 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180914-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 207
ID   ADH38512 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181643-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 208
ID   ADG83633 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180794-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 209
ID   ADH29441 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180860-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 210
ID   ADH27557 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180906-A1.
PD   25-SEP-2003.

PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 211
ID   ADH37754 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003181647-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 212
ID   ADH37931 standard; protein; 673 AA.
DE   Human secreted and transmembrane protein PRO1282.
PN   US2003181649-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 213
ID   ADH57351 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180920-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 214
ID   ADH53493 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181636-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 215
ID   ADH53663 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181641-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 216
ID   ADH51999 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181638-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 217
ID   ADH49854 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181639-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 218
ID   ADI25364 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181696-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             98.4%;   Score 3083.5;  DB 7;   Length 673;
Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 219
ID   ADH90157 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181698-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
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Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 220
ID   ADI25534 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181669-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 221
ID   ADH97708 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181672-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

RESULT 222
ID   ADI35233 standard; protein; 673 AA.
DE   Human PRO polypeptide #13.
PN   US2003050457-A1.
PD   13-MAR-2003.
Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 223
ID   ADI03556 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181656-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 224
ID   ADI11913 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181686-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 225
ID   ADH99987 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181697-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 226
ID   ADH99725 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003049682-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 227
ID   ADH98388 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181707-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 228
ID   ADI11063 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181682-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 229
ID   ADI11573 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181684-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 230
ID   ADH98218 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181709-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 231
ID   ADH98558 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181708-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 232
ID   ADH98048 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181673-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 233
ID   ADI05036 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 234
ID   ADI03386 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181654-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 235
ID   ADI04781 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181657-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 236
ID   ADH78235 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181668-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 237
ID   ADI19579 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181676-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 238
ID   ADH90327 standard; protein; 673 AA.

DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181699-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 239
ID   ADI03046 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181653-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 240
ID   ADH77895 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181666-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 241
ID   ADH97878 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181674-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 242
ID   ADI01263 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190669-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 243
ID   ADI01958 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181652-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 244
ID   ADI03216 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181655-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 245
ID   ADI11403 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181681-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 246
ID   ADI02305 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181650-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 247
ID   ADI11743 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.

PN   US2003181685-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 248
ID   ADI05380 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190716-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 249
ID   ADH79452 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003191290-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 250
ID   ADI19409 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181675-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 251
ID   ADI05210 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181677-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 252
ID   ADH79622 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003191288-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 253
ID   ADI01448 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181678-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 254
ID   ADI01618 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181679-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 255
ID   ADI01788 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181680-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Query Match   98.4%;   Score 3083.5; DB 7;   Length 673;
      Best Local Similarity   88.7%;   Pred. No. 8.1e-187;
RESULT 256
ID   ADH79792 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003191289-A1.

PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 257
ID   ADI04610 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003171550-A1.
PD   11-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 258
ID   ADI02746 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181651-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 259
ID   ADH78065 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181667-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 260
ID   ADI25704 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181670-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 261
ID   ADI25874 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181671-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 262
ID   ADK65386 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003073821-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 263
ID   ADH98728 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003191284-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 264
ID   ADH79969 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003191287-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 265
ID   ADL93700 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003040013-A1.
PD   27-FEB-2003.

PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 266
ID   ADC52154 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003130483-A1.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 267
ID   ADF35178 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2003194760-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 268
ID   ADG11428 standard; protein; 673 AA.
DE   Human PRO1282 polypeptide.
PN   US2003228665-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 269
ID   ADH06586 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180852-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 270
ID   ADH06416 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180853-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 271
ID   ADG68837 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180855-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 272
ID   ADH27727 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180912-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 273
ID   ADH25068 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180913-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 274
ID   ADH33700 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181645-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   98.4%;   Score 3083.5; DB 8; Length 673;

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       Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 275
ID   ADH02343 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180839-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 276
ID   ADH07950 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180846-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 277
ID   ADG69347 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180846-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 278
ID   ADH39168 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180917-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 279
ID   ADG83908 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180842-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 280
ID   ADH19298 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003228656-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 281
ID   ADG85452 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003166848-A1.
PD   04-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 282
ID   ADH06246 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180854-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 283
ID   ADH30076 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180856-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 293
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RESULT 284
ID   ADH24388 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180910-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 285
ID   ADG69517 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180844-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 286
ID   ADH07780 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180851-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 287
ID   ADG85792 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180861-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 288
ID   ADH39338 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180916-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 289
ID   ADH33530 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181637-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 290
ID   ADH33870 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181644-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 291
ID   ADH01080 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180838-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 292
ID   ADG69687 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180843-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               98.4%;  Score 3083.5;  DB 8;  Length 673;
     Best Local Similarity    88.7%;  Pred. No. 8.1e-187;
RESULT 293
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ID   ADH20791 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US200324358-A1
PD   04-DEC-2003.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 294
ID   ADH02173 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180841-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 295
ID   ADG69177 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180847-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 296
ID   ADG85962 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180862-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 297
ID   ADH24898 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180909-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 298
ID   ADH39515 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180915-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 299
ID   ADH19831 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein PRO1282.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 300
ID   ADH02513 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003180840-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 301
ID   ADG69007 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180849-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 302
ID   ADH07610 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.

PN   US2003180850-A1
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 303
ID   ADG86112 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180863-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 304
ID   ADH24728 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180908-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 305
ID   ADH25776 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180911-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 306
ID   ADH38342 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180922-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 307
ID   ADH57181 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181642-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 308
ID   ADH52169 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180921-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 309
ID   ADH49535 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003180857-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 310
ID   ADH90497 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181700-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   98.4%;
     Best Local Similarity   88.7%;
     Score 3083.5; DB 8; Length 673;
     Pred. No. 8.1e-187;
RESULT 311
ID   ADI11233 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003181683-A1.

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PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 312
ID   ADH98898 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190698-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 313
ID   ADI02128 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003190699-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 314
ID   ADH90667 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181701-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 315
ID   ADJ98542 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187197-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 316
ID   ADJ98712 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187228-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 317
ID   ADH78871 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181703-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 318
ID   ADJ99105 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 319
ID   ADJ99275 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 320
ID   ADJ98893 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187242-A1.
PD   02-OCT-2003.

PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 321
ID   ADH79041 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003181702-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 322
ID   ADK00901 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2003186407-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 323
ID   ADK14422 standard; protein; 673 AA.
DE   Novel human secreted and transmembrane protein PRO1282.
PN   US2003187229-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 324
ID   ADM80871 standard; protein; 673 AA.
DE   Human PRO polypeptide #8.
PN   US2004058411-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 325
ID   ADR45587 standard; protein; 673 AA.
DE   Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN   US2004176296-A1.
PD   09-SEP-2004.
PA   (MILL/) MILLENNIUM PHARM INC.
Query Match           98.4%;   Score 3083.5;   DB 8;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 326
ID   ADY77711 standard; protein; 673 AA.
DE   Neoplastic disease detection protein PRO1282.
PN   US2005059102-A1.
PD   17-MAR-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
Query Match           98.4%;   Score 3083.5;   DB 9;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 327
ID   AEA38367 standard; protein; 673 AA.
DE   Human secreted/transmembrane protein, #81.
PN   US2005112725-A1.
PD   26-MAY-2005.
PA   (GETH ) GENENTECH INC.
Query Match           98.4%;   Score 3083.5;   DB 9;   Length 673;
Best Local Similarity 88.7%;   Pred. No. 8.1e-187;

RESULT 328
ID   AAB84689 standard; protein; 673 AA.
DE   Amino acid sequence of human slit polypeptide zslit3.
PN   WO200146418-A1.
PD   28-JUN-2001.
PA   (ZYMO ) ZYMOGENETICS INC.
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Query Match        98.2%;  Score 3078.5;  DB 4;  Length 673;
Best Local Similarity  88.6%;  Pred. No. 1.7e-186;
RESULT 329
ID  ADF69108 standard; protein; 673 AA.
DE  Human MP53 protein sequence SEQ ID NO:78.
PN  WO200083047-A2.
PD  09-OCT-2003.
PA  (EXEL-) EXELIXIS INC.
Query Match        98.2%;  Score 3078.5;  DB 7;  Length 673;
Best Local Similarity  88.6%;  Pred. No. 1.7e-186;
RESULT 330
ID  ABS9449 standard; protein; 676 AA.
DE  Human genome derived single exon protein #5683.
PN  US2003194704-A1.
PD  16-OCT-2003.
PA  (PENN/) PENN S G.
PA  (RANK/) RANK D R.
PA  (HANZ/) HANZEL D K.
Query Match        98.2%;  Score 3078.5;  DB 8;  Length 676;
Best Local Similarity  88.6%;  Pred. No. 1.7e-186;
RESULT 331
ID  ADA57213 standard; protein; 672 AA.
DE  Human secreted protein #496.
PN  WO200102994-A2.
PD  27-DEC-2002.
PA  (HUMA-) HUMAN GENOME SCI INC.
Query Match        93.6%;  Score 2935;  DB 6;  Length 672;
Best Local Similarity  85.2%;  Pred. No. 2.1e-177;
RESULT 332
ID  ADA41092 standard; protein; 672 AA.
DE  Human secreted protein.
PN  WO200102993-A2.
PD  27-DEC-2002.
PA  (HUMA-) HUMAN GENOME SCI INC.
Query Match        93.6%;  Score 2935;  DB 6;  Length 672;
Best Local Similarity  85.2%;  Pred. No. 2.1e-177;
RESULT 333
ID  ABR47923 standard; protein; 672 AA.
DE  Human secreted protein, SEQ ID 814.
PN  WO200295010-A2.
PD  28-NOV-2002.
PA  (HUMA-) HUMAN GENOME SCI INC.
Query Match        93.6%;  Score 2935;  DB 6;  Length 672;
Best Local Similarity  85.2%;  Pred. No. 2.1e-177;
RESULT 334
ID  AAB38323 standard; protein; 673 AA.
DE  Human secreted protein encoded by gene 3 clone HSYAV50.
PN  WO200061623-A1.
PD  19-OCT-2000.
PA  (HUMA-) HUMAN GENOME SCI INC.
Query Match        93.6%;  Score 2935;  DB 3;  Length 673;
Best Local Similarity  85.2%;  Pred. No. 2.2e-177;
RESULT 335
ID  AAB38400 standard; peptide; 723 AA.
DE  Fragment of human secreted protein encoded by gene 3 clone HSYAV50.
PN  WO200061623-A1.
PD  19-OCT-2000.
PA  (HUMA-) HUMAN GENOME SCI INC.
Query Match        93.6%;  Score 2935;  DB 3;  Length 723;
Best Local Similarity  85.2%;  Pred. No. 2.2e-177;
RESULT 336
ID  AAU75267 standard; protein; 630 AA.
DE  Human Slit-like protein #2.
PN  WO200212346-A2.
PD  14-FEB-2002.
PA  (PHAA ) PHARMACIA CORP.
Query Match        90.8%;  Score 2845.5;  DB 5;  Length 630;
Best Local Similarity  85.2%;  Pred. No. 8.9e-172;
RESULT 337
ID  AAY66643 standard; protein; 611 AA.
DE  Membrane-bound protein PRO1282.
PN  WO963088-A2.
PD  09-DEC-1999.
PA  (GETH ) GENENTECH INC.
Query Match        86.5%;  Score 2712.5;  DB 3;  Length 611;
Best Local Similarity  79.5%;  Pred. No. 2.3e-163;
RESULT 338
ID  ABG78046 standard; protein; 673 AA.
DE  Mouse leucine-rich surface glycoprotein (LRSG-1).
PN  US2002072089-A1.
PD  13-JUN-2002.
PA  (HOLT/) HOLTZMAN D A.
PA  (MCCA/) MCCARTHY S A.
PA  (MACB/) MACBETH K J.
PA  (BUSF/) BUSFIELD S J.
PA  (PANY/) PAN Y.
PA  (WHIT/) WHITE D.
PA  (KHOD/) KHODADOUST M M.
PA  (GUWW/) GU W.
Query Match        79.4%;  Score 2490;  DB 5;  Length 673;
Best Local Similarity  73.5%;  Pred. No. 3.2e-149;
RESULT 339
ID  ADR45596 standard; protein; 673 AA.
DE  Human leucine-rich surface glycoprotein, LRSG-1, protein #2.
PN  US2004176296-A1.
PD  09-SEP-2004.
PA  (MILL-) MILLENNIUM PHARM INC.
Query Match        79.4%;  Score 2490;  DB 8;  Length 673;
Best Local Similarity  73.5%;  Pred. No. 3.2e-149;
RESULT 340
ID  ADA00753 standard; protein; 673 AA.
DE  Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.
PN  WO2003018805-A1.
PD  06-MAR-2003.
PA  (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA  (NINA-) JAPAN NAT CANCER CENT.
Query Match        79.2%;  Score 2484;  DB 6;  Length 673;
Best Local Similarity  73.4%;  Pred. No. 7.7e-149;
RESULT 341
ID  AAB07431 standard; protein; 493 AA.
DE  A leucine-rich surface glycoprotein (LRSG).
PN  WO200042170-A1.
PD  20-JUL-2000.
PA  (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match        53.3%;  Score 1672;  DB 3;  Length 493;
Best Local Similarity  53.3%;  Pred. No. 1.5e-97;
RESULT 342
ID  ABB72324 standard; protein; 281 AA.
DE  Rat protein isolated from skin cells SEQ ID NO: 648.
PN  WO200190357-A1.
PD  29-NOV-2001.
PA  (GENE-) GENESIS RES & DEV CORP LTD.
Query Match        37.6%;  Score 1178.5;  DB 5;  Length 281;
Best Local Similarity  80.7%;  Pred. No. 1.4e-66;
RESULT 343
ID  AAO30403 standard; protein; 311 AA.
DE  Human secreted protein (SECP)-6.
PN  WO2003046196-A1.
PD  05-JUN-2003.
PA  (INCY-) INCYTE GENOMICS INC.
Query Match        31.8%;  Score 997.5;  DB 7;  Length 311;
Best Local Similarity  68.7%;  Pred. No. 4.6e-55;
RESULT 344
ID  ABR58506 standard; protein; 307 AA.
DE  Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.
PN  WO2003029437-A2.
PD  10-APR-2003.
PA  (INCY-) INCYTE GENOMICS INC.
Query Match        31.3%;  Score 980.5;  DB 6;  Length 307;
Best Local Similarity  67.9%;  Pred. No. 5.5e-54;
RESULT 345
ID  AAO30821 standard; protein; 117 AA.
DE  Human cell adhesion and extracellular matrix protein (CADECM)-11.
PN  WO2003047526-A2.
PD  12-JUN-2003.
PA  (INCY-) INCYTE GENOMICS INC.
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Query Match          15.0%;    Score 471;   DB 7;   Length 117;
Best Local Similarity 98.9%;   Pred. No. 3.4e-22;
RESULT 346
ID   AAE23980 standard; protein; 635 AA.
DE   Human LP220 secreted protein.
PN   WO200226801-A2.
PD   04-APR-2002.
PA   (ELIL) LILLY & CO ELI.
Query Match          11.5%;    Score 360.5; DB 5;   Length 635;
Best Local Similarity 27.1%;   Pred. No. 2.4e-14;
RESULT 347
ID   ABP70142 standard; protein; 647 AA.
DE   Human NOV44a.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.
Query Match          11.5%;    Score 360.5; DB 5;   Length 647;
Best Local Similarity 27.1%;   Pred. No. 2.5e-14;
RESULT 348
ID   AAO26256 standard; protein; 635 AA.
DE   MDDT related human protein SEQ ID No 34.
PN   WO200296951-A1.
PD   05-DEC-2002.
PA   (INCY) INCYTE GENOMICS INC.
Query Match          11.5%;    Score 359.5; DB 6;   Length 635;
Best Local Similarity 27.6%;   Pred. No. 2.8e-14;
RESULT 349
ID   ADZ09859 standard; protein; 635 AA.
DE   Human breast cancer marker MGC3103 protein.
PN   EP1522594-A2.
PD   13-APR-2005.
PA   (FARB ) BAYER HEALTHCARE AG.
Query Match          11.5%;    Score 359.5; DB 9;   Length 635;
Best Local Similarity 27.6%;   Pred. No. 2.8e-14;
RESULT 350
ID   ABP70144 standard; protein; 778 AA.
DE   Human NOV44c.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.
Query Match          11.4%;    Score 357.5; DB 5;   Length 778;
Best Local Similarity 26.7%;   Pred. No. 4.8e-14;
RESULT 351
ID   ADM90979 standard; protein; 545 AA.
DE   Human pharmaceutically useful protein SeqID 372.
PN   WO2004020595-A2.
PD   11-MAR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA   (RIKE) RIKEN INST PHYSICAL & CHEM RES.
PA   (DNAF-) DNAFORM KK.
Query Match          11.2%;    Score 350.5; DB 8;   Length 545;
Best Local Similarity 27.9%;   Pred. No. 8.7e-14;
RESULT 352
ID   ABP70143 standard; protein; 566 AA.
DE   Human NOV44b.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.
Query Match          10.8%;    Score 339;   DB 5;   Length 566;
Best Local Similarity 26.9%;   Pred. No. 4.9e-13;
RESULT 353
ID   AAE17484 standard; protein; 551 AA.
DE   Human leucine-rich repeat-8 (ZLRR8) protein #2.
PN   WO200220604-A2.
PD   10-JAN-2002.
PA   (ZYMO ) ZYMOGENETICS INC.
Query Match          10.8%;    Score 338;   DB 5;   Length 551;
Best Local Similarity 27.4%;   Pred. No. 5.5e-13;
RESULT 354
ID   ADI21104 standard; protein; 618 AA.
DE   Novel human protein #79.
PN   WO2003025148-A2.
PD   27-MAR-2003.

PA   (HYSE-) HYSEQ INC.
Query Match          10.7%;    Score 337;   DB 7;   Length 618;
Best Local Similarity 27.2%;   Pred. No. 7.2e-13;
RESULT 355
ID   ADA23287 standard; protein; 653 AA.
DE   Human SECX polypeptide, SEC5 #1.
PN   US2003054514-A1.
PD   20-MAR-2003.
PA   (SHIM/) SHIMKETS R A.
PA   (LARO/) LAROCHELLE W J.
Query Match          10.7%;    Score 337;   DB 6;   Length 653;
Best Local Similarity 23.6%;   Pred. No. 7.7e-13;
RESULT 356
ID   AAB23033 standard; protein; 694 AA.
DE   Human SLIT protein-like splice variant, SECX 3352358-1.
PN   WO200053742-A2.
PD   14-SEP-2000.
PA   (CURA-) CURAGEN CORP.
Query Match          10.7%;    Score 337;   DB 3;   Length 694;
Best Local Similarity 23.6%;   Pred. No. 8.3e-13;
RESULT 357
ID   AAB23034 standard; protein; 590 AA.
DE   Human SLIT protein-like splice variant, SECX 3352358-2.
PN   WO200053742-A2.
PD   14-SEP-2000.
PA   (CURA-) CURAGEN CORP.
Query Match          10.6%;    Score 333;   DB 3;   Length 590;
Best Local Similarity 25.8%;   Pred. No. 1.2e-12;
RESULT 358
ID   ADA23289 standard; protein; 590 AA.
DE   Human SECX polypeptide, SEC6.
PN   US2003054514-A1.
PD   20-MAR-2003.
PA   (SHIM/) SHIMKETS R A.
PA   (LARO/) LAROCHELLE W J.
Query Match          10.6%;    Score 333;   DB 6;   Length 590;
Best Local Similarity 25.8%;   Pred. No. 1.2e-12;
RESULT 359
ID   ABG04827 standard; protein; 526 AA.
DE   Novel human diagnostic protein #4818.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match          10.6%;    Score 332;   DB 4;   Length 526;
Best Local Similarity 26.9%;   Pred. No. 1.2e-12;
RESULT 360
ID   AAY28806 standard; protein; 653 AA.
DE   cc359_4 secreted protein.
PN   WO9950405-A1.
PD   07-OCT-1999.
PA   (GEMY ) GENETICS INST INC.
Query Match          10.5%;    Score 330;   DB 2;   Length 653;
Best Local Similarity 24.2%;   Pred. No. 2.1e-12;
RESULT 361
ID   AAY66694 standard; protein; 653 AA.
DE   Membrane-bound protein PRO1111.
PN   WO9963088-A2.
PD   09-DEC-1999.
PA   (GETH ) GENENTECH INC.
Query Match          10.5%;    Score 330;   DB 3;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 362
ID   AAB24073 standard; protein; 653 AA.
DE   Human PRO1111 protein sequence SEQ ID NO:46.
PN   WO200053755-A2.
PD   14-SEP-2000.
PA   (GETH ) GENENTECH INC.
Query Match          10.5%;    Score 330;   DB 3;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 363
ID   AAU12390 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide sequence.
PN   WO200140466-A2.
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PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 4; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 364
ID   AAE09438 standard; protein; 653 AA.
DE   Human sbgPRO331a protein.
PN   WO200160850-A1.
PD   23-AUG-2001.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match          10.5%;  Score 330; DB 4; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 365
ID   AAB65217 standard; protein; 653 AA.
DE   Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 4; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 366
ID   ABU58032 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003027163-A1.
PD   06-FEB-2003.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 367
ID   ABU59110 standard; protein; 653 AA.
DE   Novel human secreted or transmembrane protein PRO1111.
PN   US200213252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 368
ID   ABU82622 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003032023-A1.
PD   13-FEB-2003.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 369
ID   ABO17834 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US200303156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 370
ID   ABU60541 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein, #93.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 371
ID   ABU13923 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2002103125-A1.
PD   01-AUG-2002.
PA   (GETH ) GENENTECH LTD.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 372
ID   ABU81088 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.

     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 373
ID   ABU72508 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003003531-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 374
ID   ABU66788 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 375
ID   AAO23105 standard; protein; 653 AA.
DE   NAG14 'human modifier of p53 pathway' protein.
PN   WO2003035833-A2.
PD   01-MAY-2003.
PA   (EXEL-) EXELIXIS INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 376
ID   ABU59869 standard; protein; 653 AA.
DE   Novel secreted and transmembrane protein PRO1111.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 377
ID   ABU59257 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein, #93.
PN   US2003027162-A1.
PD   06-FEB-2003.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 378
ID   ABO25954 standard; protein; 653 AA.
DE   Human PRO1111 polypeptide.
PN   US2002127576-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 379
ID   ABO25059 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein (PRO) #219.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 380
ID   ABU58963 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein, #93.
PN   US2002142961-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 381
ID   ABU92341 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003022187-A1.
PD   30-JAN-2003.
     Query Match          10.5%;  Score 330; DB 6; Length 653;
     Best Local Similarity 24.3%; Pred. No. 653 AA.
RESULT 382
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ID   ABU59406 standard; protein;  653 AA.
DE   Novel human secreted or transmembrane protein PRO1344.
PN   US2003027985-A1.
PD   06-FEB-2003.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 383
ID   ABU67064 standard; protein;  653 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 438.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 384
ID   ABU92172 standard; protein;  653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003017476-A1.
PD   23-JAN-2003.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 385
ID   ABU10878 standard; protein;  653 AA.
DE   Human PRO polypeptide #64.
PN   US2002123463-A1.
PD   05-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 386
ID   ABU81630 standard; protein;  653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2002177164-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 387
ID   ABU88569 standard; protein;  653 AA.
DE   Human secreted and transmembrane polypeptide PRO1111.
PN   US2002197615-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 388
ID   ABO34083 standard; protein;  653 AA.
DE   Human PRO1111 polypeptide.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 389
ID   ADA45957 standard; protein;  653 AA.
DE   Human PRO polypeptide #219.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 390
ID   ADA76388 standard; protein;  653 AA.
DE   Human PRO polypeptide #219.
PN   US2003073212-A1.
PD   17-APR-2003.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 391
ID   ADA19038 standard; protein;  653 AA.
DE   Human PRO polypeptide #219.
PN   US2003054517-A1.
PD   20-MAR-2003.

PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 392
ID   ADA61661 standard; protein;  653 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 393
ID   ADB19446 standard; protein;  653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 394
ID   ADB27987 standard; protein;  653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 395
ID   ADA86466 standard; protein;  653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 396
ID   ADB16030 standard; protein;  653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 397
ID   ADA37740 standard; protein;  653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 398
ID   ADA47816 standard; protein;  653 AA.
DE   Human PRO polypeptide #219.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 399
ID   ADA21426 standard; protein;  653 AA.
DE   Human secreted/transmembrane polypeptide PRO1111.
PN   US2003054404-A1.
PD   20-MAR-2003.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 400
ID   ADA10213 standard; protein;  653 AA.
DE   Human secreted/transmembrane protein, PRO1111.
PN   US2003059831-A1.
PD   27-MAR-2003.
     Query Match             10.5%;   Score 330;  DB 6;   Length 653;
     Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
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RESULT 401
ID ADA67611 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 402
ID ADB30618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 403
ID ADA85914 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 404
ID ADA17757 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 405
ID ADA97126 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 406
ID ADA79430 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 407
ID ADA87569 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 408
ID ADB16771 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 409
ID ADA27865 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 410
ID ADA91863 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 411
ID ADB14926 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 412
ID ADB18887 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 413
ID ADA94102 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 414
ID ADB19998 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 415
ID ADB13310 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 416
ID ABO43367 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 417
ID ADA94445 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 418
ID ADA74564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   10.5%; Score 330; DB 6; Length 653;
  Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 419
ID ADB24797 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077713-A1.
PD 24-APR-2003.

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PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 420
ID      ADA82321 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003082701-A1.
PD      01-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 421
ID      ADA75284 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003073216-A1.
PD      17-APR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 422
ID      ADA85362 standard; protein; 653 AA.
DE      Novel human secreted and transmembrane protein PRO1111.
PN      US2003082695-A1.
PD      01-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 423
ID      ADA84810 standard; protein; 653 AA.
DE      Novel human secreted and transmembrane protein PRO1111.
PN      US2003082708-A1.
PD      01-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 424
ID      ADB30066 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003073214-A1.
PD      17-APR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 425
ID      ADA80594 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003082761-A1.
PD      01-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 426
ID      ADA75836 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003082703-A1.
PD      01-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 427
ID      ADA38670 standard; protein; 653 AA.
DE      Human secreted/transmembrane protein PRO1111.
PN      US2003059780-A1.
PD      27-MAR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 428
ID      ADA47061 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003073210-A1.
PD      17-APR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;


        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 429
ID      ADB25357 standard; protein; 653 AA.
DE      Human PRO polypeptide SEQ ID NO 438.
PN      US2003077715-A1.
PD      24-APR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 430
ID      ADA93533 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003077721-A1.
PD      24-APR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 431
ID      ADB26883 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003092147-A1.
PD      15-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 432
ID      ADB31170 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003096386-A1.
PD      22-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 433
ID      ADA92791 standard; protein; 653 AA.
DE      Human secreted/transmembrane protein PRO1111.
PN      US2003060407-A1.
PD      27-MAR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 434
ID      ADA61098 standard; protein; 653 AA.
DE      Homo sapiens.
PN      US2003049817-A1.
PD      13-MAR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 435
ID      ADB24245 standard; protein; 653 AA.
DE      Human PRO polypeptide SEQ ID NO 438.
PN      US2003077714-A1.
PD      24-APR-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 436
ID      ADA96574 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003082690-A1.
PD      01-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 437
ID      ADA81146 standard; protein; 653 AA.
DE      Human PRO polypeptide #219.
PN      US2003082702-A1.
PD      01-MAY-2003.
PA      (GETH ) GENENTECH INC.
        Query Match              10.5%;    Score 330;   DB 6;   Length 653;
        Best Local Similarity    24.3%;    Pred. No. 2.1e-12;
RESULT 438
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ID   ADA96022 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 6;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 439
ID   ADB26331 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 6;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 440
ID   ADB21816 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 6;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 441
ID   ADA77595 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 442
ID   ADB18835 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 443
ID   ADA87018 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 444
ID   ADA88121 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 445
ID   ADA46509 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 446
ID   ADB28539 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 447
ID   ADB29091 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 448
ID   ADO53169 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003044806-A1.
PD   06-MAR-2003.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 449
ID   ADA77043 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 450
ID   ADA22352 standard; protein; 653 AA.
DE   Human secreted/transmembrane polypeptide PRO1111.
PN   US2003040473-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 451
ID   ADA88673 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 452
ID   ADA97678 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 453
ID   ADB27435 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003022239-A1.
PD   30-JAN-2003.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 454
ID   ADA22368 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087344-A1.
PD   08-MAY-2003.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 455
ID   ABO22539 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003017982-A1.
PD   23-JAN-2003.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 456
ID   ADA06518 standard; protein; 653 AA.
DE   Human secreted/transmembrane PRO polypeptide #64.
PN   US2003049638-A1.
PD   13-MAR-2003.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 457
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ID   ADA39211 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003059782-A1.
PD   27-MAR-2003.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 458
ID   ADA67059 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 459
ID   ADB22920 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 460
ID   ADB23693 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 461
ID   ADA92415 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 462
ID   ADB15478 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 463
ID   ADB38730 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 464
ID   ADB96237 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003054403-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 465
ID   ADB38178 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087347-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 466
ID   ADB66650 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 467
ID   ADB89730 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 468
ID   ADB90462 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 469
ID   ADB39563 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 470
ID   ADB47186 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 471
ID   ADB86793 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 472
ID   ADB77398 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 473
ID   ADB34555 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 474
ID   ADB35659 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score  330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;
                             Pred. No. 2.1e-12;
RESULT 475
ID   ADB34003 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077716-A1.
PD   24-APR-2003.
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PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 476
ID   ADB35107 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 477
ID   ADB36211 standard; protein; 653 AA.
DE   Human PRO polypeptide SEQ ID NO 438.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 478
ID   ADB46606 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 479
ID   ADC57709 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003027754-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 480
ID   ADC55073 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003045463-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 481
ID   ADC11940 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003049681-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 482
ID   ADC56362 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003064375-A1.
PD   03-APR-2003.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 483
ID   ADC07417 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003068647-A1.
PD   10-APR-2003.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 484
ID   ADC11407 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003069403-A1.
PD   10-APR-2003.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 485
ID   ADC50479 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092106-A1.
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PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 486
ID   ADC72026 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 487
ID   ADC60005 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 488
ID   ADC53012 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 489
ID   ADC57366 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 490
ID   ADC60557 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 491
ID   ADC51032 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 492
ID   ADC65559 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 493
ID   ADC54657 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 494
ID   ADC53618 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087364-A1.
PD   08-MAY-2003.
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PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 495
ID   ADC59141 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 496
ID   ADC56019 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 497
ID   ADC58589 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein Seq ID438.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 498
ID   ADC14529 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003082546-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 499
ID   ADD08061 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003068623-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 500
ID   ADD03263 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 501
ID   ADC90255 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 502
ID   ADC81886 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003083461-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 503
ID   ADC69674 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 504

ID   ADC48563 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 505
ID   ADD10092 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 506
ID   ADD07528 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 507
ID   ADD04667 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 508
ID   ADC82419 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003059833-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 509
ID   ADC80623 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 510
ID   ADD11130 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 511
ID   ADC48011 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 512
ID   ADD08599 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003073090-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330;   DB 7;   Length 653;
Best Local Similarity 24.3%;   Pred. No. 2.1e-12;
RESULT 513
ID   ADC80071 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087358-A1.

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PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 514
ID   ADD06848 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2002219300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 515
ID   ADD09540 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003059775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 516
ID   ADC83095 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003059783-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 517
ID   ADD41253 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 518
ID   ADD52392 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 519
ID   ADD53132 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 520
ID   ADD55684 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 521
ID   ADD55202 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077593-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 522
ID   ADD56160 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2003077594-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;

RESULT 523
ID   ADD51840 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 524
ID   ADD02639 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 525
ID   ADD02073 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 526
ID   ADD54255 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003203432-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 527
ID   ADD54598 standard; protein; 653 AA.
DE   Human PRO polypeptide #64.
PN   US2002132255-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 528
ID   ADD92572 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 529
ID   ADD91468 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 530
ID   ADE04082 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 531
ID   ADE26752 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087304-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. No. 2.1e-12;
RESULT 532
ID   ADE32379 standard; protein; 653 AA.
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DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 533
ID   ADE22311 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 534
ID   ADD79535 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 535
ID   ADE42071 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 536
ID   ADE17888 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 537
ID   ADD92020 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 538
ID   ADE33483 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 539
ID   ADE34035 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 540
ID   ADD80087 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 541
ID   ADD93124 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.

PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 542
ID   ADE19544 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 543
ID   ADE18992 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 544
ID   ADE43188 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 545
ID   ADD95977 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 546
ID   ADE22863 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 547
ID   ADD78981 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 548
ID   ADE26219 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003087305-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 549
ID   ADE32931 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.5%;  Score 330;  DB 7;  Length 653;
     Best Local Similarity   24.3%;  Pred. 653 AA.
RESULT 550
ID   ADE42623 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003199032-A1.
PD   23-OCT-2003.
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PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 551
ID ADD80639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 552
ID ADD89667 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 553
ID ADE40951 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 554
ID ADE04750 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 555
ID ADE92879 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 556
ID ADF67156 standard; protein; 653 AA.
DE Human PRO1111 amino acid sequence SEQ ID NO:229.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 557
ID ADG21588 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 558
ID ADG23229 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 559
ID ADF97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 560
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 561
ID ADG80076 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 562
ID ADH55368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 563
ID ADH55920 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 564
ID ADI35410 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 565
ID ADI64139 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 566
ID ADI65088 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 567
ID ADI63587 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 568
ID ADH82001 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   10.5%;   Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;

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RESULT 569
ID ADH99902 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003049682-A1.
PD 13-MAR-2003.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 570
ID ADH81449 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 571
ID ADM82618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 572
ID ADN16017 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 573
ID ADN16646 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 574
ID ADN15465 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 575
ID ADN14913 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 576
ID ADC81175 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 577
ID ADD76623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 578
ID ADD87987 standard; protein; 653 AA.

DE Human PRO polypeptide #219.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 579
ID ADD86391 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 580
ID ADE75839 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003211571-A1.
PD 13-NOV-2003.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 581
ID ADE23415 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 582
ID ADE23967 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 583
ID ADE24610 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 584
ID ADD87435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 585
ID ADE89301 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 586
ID ADE18440 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 8; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 587
ID ADE88749 standard; protein; 653 AA.
DE Human PRO polypeptide #219.

PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 588
ID ADE94769 standard; protein; 653 AA.
DE Human PRO1111 polypeptide #219.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 589
ID ADE91180 standard; protein; 653 AA.
DE Human PRO1111 polypeptide #219.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 590
ID ADF35355 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 591
ID ADE95321 standard; protein; 653 AA.
DE Human PRO1111 polypeptide #219.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 592
ID ADE93431 standard; protein; 653 AA.
DE Human PRO1111 polypeptide #219.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 593
ID ADF35012 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 594
ID ADE92327 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 595
ID ADE90628 standard; protein; 653 AA.
DE Human PRO1111 polypeptide #219.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 596
ID ADE91775 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199058-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 597
ID ADG1605 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 598
ID ADG02354 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 599
ID ADG22140 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 600
ID ADG20210 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 601
ID ADF98116 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 602
ID ADG24333 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 603
ID ADF98687 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 604
ID ADG03518 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
    Query Match   10.5%; Score 330; DB 8; Length 653;
    Best Local Similarity   24.3%; Pred. No. 2.1e-12;
RESULT 605
ID ADF99239 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

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Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 606
ID   ADG16824 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 607
ID   ADG05283 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 608
ID   ADG19550 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 609
ID   ADG13387 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 610
ID   ADG08444 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 611
ID   ADG15614 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 612
ID   ADF97012 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 613
ID   ADG06197 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 614
ID   ADG23781 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;

Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 615
ID   ADG04070 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 616
ID   ADG24971 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 617
ID   ADG07268 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 618
ID   ADG07820 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 619
ID   ADG55315 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 620
ID   ADG60979 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 621
ID   ADG62083 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 622
ID   ADG82284 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
RESULT 623
ID   ADG57523 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;   Score 330;  DB 8;  Length 653;
Best Local Similarity   24.3%;   Pred. No. 2.1e-12;
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RESULT 624
ID   ADG56971 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 625
ID   ADG55867 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 626
ID   ADG58627 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 627
ID   ADG70993 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 628
ID   ADG58075 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 629
ID   ADG53659 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 630
ID   ADG71545 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 631
ID   ADG81732 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 632
ID   ADH19475 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003228656-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 633
ID   ADH30694 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 634
ID   ADH12061 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 635
ID   ADG52483 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 636
ID   ADG54211 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 637
ID   ADG81180 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 638
ID   ADG56419 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 639
ID   ADH12685 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 640
ID   ADH20968 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003224358-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 641
ID   ADG61531 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653;
     Best Local Similarity   24.3%; Pred. No. 2.1e-12;

RESULT 642
ID   ADH20008 standard; protein; 653 AA.
DE   Human secreted/transmembrane protein PRO1111.
PN   US2003219856-A1.

PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 643
ID   ADH28618 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003022231-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 644
ID   ADG54763 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 645
ID   ADG59803 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 646
ID   ADI81227 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 647
ID   ADG09970 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 648
ID   ADI15441 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 649
ID   ADG09318 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 650
ID   ADI14773 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 651
ID   ADI18368 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207349-A1.
PD   06-NOV-2003.

PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 652
ID   ADJ63649 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 653
ID   ADJ77544 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004038336-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 654
ID   ADJ65666 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 655
ID   ADM27802 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 656
ID   ADM42526 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 657
ID   ADM28388 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 658
ID   ADI95870 standard; protein; 653 AA.
DE   Human PRO polypeptide #219.
PN   US2003077659-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 659
ID   ADI96422 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2003207354-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%; Score 330; DB 8; Length 653
     Best Local Similarity   24.3%;
RESULT 660
ID   ADS32374 standard; protein; 653 AA.
DE   Novel human secreted and transmembrane protein PRO1111.
PN   US2004203125-A1.
PD   14-OCT-2004.
PA   (GETH) GENENTECH INC.

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Query Match          10.5%;  Score 330;  DB 8;  Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 661
ID  ADT03358 standard; protein; 653 AA.
DE  Human PRO polypeptide #219.
PN  US2004214269-A1.
PD  28-OCT-2004.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 330;  DB 8;  Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 662
ID  AD203409 standard; protein; 653 AA.
DE  Human secreted/transmembrane PRO1111 protein.
PN  US2005074837-A1.
PD  07-APR-2005.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 330;  DB 9;  Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 663
ID  AEA38492 standard; protein; 653 AA.
DE  Human secreted/transmembrane protein, #132.
PN  US2005112725-A1.
PD  26-MAY-2005.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 330;  DB 9;  Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 664
ID  AEA23332 standard; protein; 653 AA.
DE  Tumor antigen of hematopoietic origin TAHO15.
PN  WO2005049075-A2.
PD  02-JUN-2005.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 330;  DB 9;  Length 653;
Best Local Similarity  24.3%;  Pred. No. 2.1e-12;
RESULT 665
ID  AEB14155 standard; protein; 653 AA.
DE  Cancer cell diagnosis method-related human protein - SEQ ID 438.
PN  US2005153396-A1.
PD  14-JUL-2005.
PA  (BAKE/) BAKER K P.
PA  (BERE/) BERESINI M.
PA  (DEFO/) DEFORGE L.
PA  (DESN/) DESNOYERS L.
PA  (FILV/) FILVAROFF E.
PA  (GAOW/) GAO W.
PA  (GERR/) GERRITSEN M E.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (SHER/) SHERWOOD S.
PA  (SMIT/) SMITH V.
PA  (STEW/) STEWART T A.
PA  (TUMA/) TUMAS D.
PA  (WATA/) WATANABE C K.
PA  (WOOD/) WOOD W I.
PA  (ZHAN/) ZHANG Z.
RESULT 666
ID  ABU12069 standard; protein; 775 AA.
DE  Human NOV15a CG92531-01 protein SEQ ID 58.
PN  WO200281625-A2.
PD  17-OCT-2002.
PA  (CURA-) CURAGEN CORP.
Query Match          10.5%;  Score 329.5;  DB 6;  Length 775;
Best Local Similarity  26.0%;  Pred. No. 2.8e-12;
RESULT 667
ID  ABG98014 standard; protein; 649 AA.
DE  Human leucine rich repeat domain protein associated protein #1.
PN  WO200274959-A2.
PD  26-SEP-2002.
PA  (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match          10.5%;  Score 329;  DB 5;  Length 649;

Best Local Similarity  24.6%;  Pred. No. 2.5e-12;
RESULT 668
ID  ADS98753 standard; protein; 824 AA.
DE  Protein factor discovery related human contig polypeptide, SEQ ID 1017.
PN  WO2004087874-A2.
PD  14-OCT-2004.
PA  (NUVE-) NUVELO INC.
PA  (DRMA/) DRMANAC R T.
Query Match          10.5%;  Score 329;  DB 8;  Length 824;
Best Local Similarity  25.5%;  Pred. No. 3.3e-12;
RESULT 669
ID  ABG34079 standard; protein; 627 AA.
DE  Human Pro peptide #51.
PN  WO20024888-A2.
PD  28-MAR-2002.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 5;  Length 627;
Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 670
ID  ADA01368 standard; protein; 627 AA.
DE  Human PRO polypeptide #50.
PN  US2003068779-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 6;  Length 627;
Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 671
ID  ADA43797 standard; protein; 627 AA.
DE  Human secreted/transmembrane polypeptide PRO34192.
PN  US2003064474-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 6;  Length 627;
Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 672
ID  ADA43565 standard; protein; 627 AA.
DE  Human secreted/transmembrane polypeptide PRO34192
PN  US2003073196-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 6;  Length 627;
Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 673
ID  ADA01240 standard; protein; 627 AA.
DE  Human PRO polypeptide #50.
PN  US2003068782-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 6;  Length 627;
Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 674
ID  ADA01124 standard; protein; 627 AA.
DE  Human secreted/transmembrane polypeptide PRO34192.
PN  US2003068780-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 7;  Length 627;
Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 675
ID  ADA43681 standard; protein; 627 AA.
DE  Human secreted/transmembrane polypeptide PRO34192.
PN  US2003073190-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 7;  Length 627;
Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 676
ID  ADA06943 standard; protein; 627 AA.
DE  Human PRO polypeptide #50.
PN  US2003068781-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          10.5%;  Score 328.5;  DB 7;  Length 627;
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Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 677
ID   ADA08431 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003066783-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 678
ID   ADB99724 standard; protein; 627 AA.
DE   Human PRO polypeptide SEQ ID 100.
PN   US2003082726-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 679
ID   ADB87007 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003082726-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 680
ID   ADB66162 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003082729-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 681
ID   ADB99840 standard; protein; 627 AA.
DE   Human PRO polypeptide SEQ ID 100.
PN   US2003073192-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 682
ID   ADB99495 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003082731-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 683
ID   ADB66046 standard; protein; 627 AA.
DE   Human secreted/transmembrane PRO polypeptide (SeqID 100).
PN   US2003082732-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 684
ID   ADC23444 standard; protein; 627 AA.
DE   Human transmembrane PRO polypeptide (SeqID 100).
PN   US2003073193-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 685
ID   ADC26137 standard; protein; 627 AA.
DE   Human PRO34192 protein.
PN   US2003073194-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;

RESULT 686
ID   ADE04964 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003068778-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 687
ID   ADE11270 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003073191-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 688
ID   ADD88201 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003082733-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 689
ID   ADD95496 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003064473-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 690
ID   ADE06426 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003073195-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 691
ID   ADE38201 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119120-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 692
ID   ADD88317 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003073189-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 693
ID   ADD90898 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003073188-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 694
ID   ADF99453 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003078401-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.5%;    Score 328.5; DB 7;    Length 627;
Best Local Similarity    24.2%;    Pred. No. 2.5e-12;
RESULT 695
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ID   ADG06546 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003077742-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 7;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 696
ID   ADG05497 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003077741-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 7;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 697
ID   ADG82498 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003077744-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 7;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 698
ID   ADE51751 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104560-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 699
ID   ADE51867 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104561-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 700
ID   ADE37725 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104564-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 701
ID   ADE37609 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104565-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 702
ID   ADD95380 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138901-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 703
ID   ADE38080 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003104556-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 704
ID   ADE76169 standard; protein; 627 AA.

DE   Human PRO polypeptide #50.
PN   US2003124665-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 705
ID   ADE39492 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119117-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 706
ID   ADE04296 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003096364-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 707
ID   ADE39893 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003118896-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 708
ID   ADE19758 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138903-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 709
ID   ADE77336 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003124666-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 710
ID   ADE65444 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119116-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 711
ID   ADE76053 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003124663-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 712
ID   ADE37964 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119119-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match    10.5%;   Score 328.5;  DB 8;   Length 627;
Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 713
ID   ADE64574 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
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PN   US2003119114-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 714
ID   ADE38909 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003096363-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 715
ID   ADE51983 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104562-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 716
ID   ADD91014 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003138902-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 717
ID   ADE38793 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003108996-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 718
ID   ADE37493 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104563-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 719
ID   ADE06309 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138898-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 720
ID   ADD90169 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003138904-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 721
ID   ADE38677 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119086-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 722
ID   ADE39608 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119118-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 723
ID   ADD89213 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138897-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 724
ID   ADD88980 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138899-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 725
ID   ADE19874 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003138900-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 726
ID   ADE77452 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003124667-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 727
ID   ADE65328 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119113-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 728
ID   ADE39376 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119115-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 729
ID   ADE38561 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003170809-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 730
ID   ADG11114 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003104559-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;  Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 731
ID   ADG10998 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003077743-A1.
PD   24-APR-2003.
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PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 732
ID   ADH31526 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119139-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 733
ID   ADH38774 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119140-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 734
ID   ADH29909 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119137-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 735
ID   ADH23712 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119143-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 736
ID   ADH27042 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119135-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 737
ID   ADH38310 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119124-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 738
ID   ADH26926 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119134-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 739
ID   ADH38194 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119123-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 740
ID   ADH38890 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119141-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.

     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 741
ID   ADH23828 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119142-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 742
ID   ADH40203 standard; protein; 627 AA.
DE   Human PRO34192 protein.
PN   US2003119132-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 743
ID   ADH40088 standard; protein; 627 AA.
DE   Human PRO34192 protein.
PN   US2003119133-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 744
ID   ADH31410 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003119118-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 745
ID   ADH29288 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003119136-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 746
ID   ADH49503 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119127-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 747
ID   ADH51967 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119125-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 748
ID   ADH49822 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119128-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;
     Best Local Similarity 24.2%;   Pred. No. 2.5e-12;
RESULT 749
ID   ADH52423 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119130-A1.
PD   26-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.5%;   Score 328.5; DB 8;   Length 627;

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     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 750
ID   ADH52539 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119129-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;   Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 751
ID   ADH58536 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119121-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;   Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 752
ID   ADH51851 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119126-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;   Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 753
ID   ADH58412 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119122-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;   Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 754
ID   ADI13609 standard; protein; 627 AA.
DE   Novel human secreted and transmembrane protein PRO34192.
PN   US2003119131-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;   Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 755
ID   ADK00865 standard; protein; 627 AA.
DE   Human PRO polypeptide #50.
PN   US2003186373-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;   Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 756
ID   ADL08606 standard; protein; 627 AA.
DE   Human secreted/transmembrane polypeptide PRO34192.
PN   US2003186372-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        10.5%;   Score 328.5;  DB 8;  Length 627;
     Best Local Similarity  24.2%;  Pred. No. 2.5e-12;
RESULT 757
ID   AAU32870 standard; protein; 636 AA.
DE   Human secreted protein #3361.
PN   WO200179449-A2.
PD   25-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match        10.4%;   Score 327.5;  DB 4;  Length 636;
     Best Local Similarity  24.2%;  Pred. No. 3e-12;
RESULT 758
ID   AB084499 standard; protein; 626 AA.
DE   Mouse cancer-associated protein MP14-035.1.
PN   WO200074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match        10.3%;   Score 324;  DB 8;  Length 626;
     Best Local Similarity  24.3%;  Pred. No. 4.9e-12;


RESULT 759
ID   AAG65805 standard; protein; 628 AA.
DE   Human leucine-rich repeat (LRR) family member, 33395 polypeptide.
PN   WO200172827-A2.
PD   04-OCT-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match        10.3%;   Score 324;  DB 4;  Length 628;
     Best Local Similarity  24.1%;  Pred. No. 4.9e-12;
RESULT 760
ID   ADN95165 standard; protein; 810 AA.
DE   Human BEC/LEC-related protein sequence SeqID87.
PN   WO2003080640-A1.
PD   02-OCT-2003.
PA   (LUDW-) LUDWIG INST CANCER RES.
     (LICN ) LICENTIA LTD.
     Query Match        10.3%;   Score 322.5;  DB 7;  Length 810;
     Best Local Similarity  22.0%;  Pred. No. 8.2e-12;
RESULT 761
ID   ABR58642 standard; protein; 811 AA.
DE   Human cancer related protein SEQ ID NO:299.
PN   WO2003025138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match        10.3%;   Score 322.5;  DB 6;  Length 811;
     Best Local Similarity  22.0%;  Pred. No. 8.3e-12;
RESULT 762
ID   AAO23114 standard; protein; 811 AA.
DE   KIAA0644 'human modifier of p53 pathway' protein.
PN   WO2003035833-A2.
PD   01-MAY-2003.
PA   (EXEL-) EXELIXIS INC.
     Query Match        10.3%;   Score 322.5;  DB 6;  Length 811;
     Best Local Similarity  22.0%;  Pred. No. 8.3e-12;
RESULT 763
ID   ADN95110 standard; protein; 811 AA.
DE   Human LEC protein sequence SeqID32.
PN   WO2003080640-A1.
PD   02-OCT-2003.
PA   (LUDW-) LUDWIG INST CANCER RES.
     (LICN ) LICENTIA LTD.
     Query Match        10.3%;   Score 322.5;  DB 7;  Length 811;
     Best Local Similarity  22.0%;  Pred. No. 8.3e-12;
RESULT 764
ID   ADQ21196 standard; protein; 811 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match        10.3%;   Score 322.5;  DB 8;  Length 811;
     Best Local Similarity  22.0%;  Pred. No. 8.3e-12;
RESULT 765
ID   ADR45590 standard; protein; 605 AA.
DE   Homologue of LRSG-1, baboon ALS.
PN   US2004176296-A1.
PD   09-SEP-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match        10.3%;   Score 322;  DB 8;  Length 605;
     Best Local Similarity  36.2%;  Pred. No. 6.3e-12;
RESULT 766
ID   AAG67523 standard; protein; 628 AA.
DE   Amino acid sequence of a human secreted polypeptide.
PN   WO200166690-A2.
PD   13-SEP-2001.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
     (SMIK ) SMITHKLINE BEECHAM PLC.
     Query Match        10.2%;   Score 321;  DB 4;  Length 628;
     Best Local Similarity  23.9%;  Pred. No. 7.6e-12;
RESULT 767
ID   AAB84469 standard; protein; 628 AA.
DE   Amino acid sequence of an interferon omega-1 like protein NOV2.
PN   WO200142471-A2.
PD   14-JUN-2001.
PA   (CURA-) CURAGEN CORP.
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Query Match            10.2%;   Score 321;  DB 4;  Length 628;
Best Local Similarity  23.9%;   Pred. No. 7.6e-12;
RESULT 768
ID   ABP69326 standard; protein; 628 AA.
DE   Human polypeptide SEQ ID NO 1373.
PN   WO200270539-A2.
PD   12-SEP-2002.
PA   (HYSE-) HYSEQ INC.
RESULT 769
ID   ADF69107 standard; protein; 628 AA.
DE   Human MP53 protein sequence SEQ ID NO:77.
PN   WO200308047-A2.
PD   09-OCT-2003.
PA   (EXEL-) EXELIXIS INC.
Query Match            10.2%;   Score 321;  DB 5;  Length 628;
Best Local Similarity  23.9%;   Pred. No. 7.6e-12;
RESULT 770
ID   ADH71652 standard; protein; 628 AA.
DE   Human protein of the invention NOV22a SEQ ID NO:548.
PN   WO200102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Query Match            10.2%;   Score 321;  DB 7;  Length 628;
Best Local Similarity  23.9%;   Pred. No. 7.6e-12;
RESULT 771
ID   ADH71654 standard; protein; 628 AA.
DE   Human protein of the invention NOV22b SEQ ID NO:550.
PN   WO200102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Query Match            10.2%;   Score 321;  DB 8;  Length 628;
Best Local Similarity  23.9%;   Pred. No. 7.6e-12;
RESULT 772
ID   ABO84502 standard; protein; 628 AA.
DE   Human cancer-associated protein HP14-035.3.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Query Match            10.2%;   Score 321;  DB 8;  Length 628;
Best Local Similarity  23.9%;   Pred. No. 7.6e-12;
RESULT 773
ID   ABO84503 standard; protein; 628 AA.
DE   Human cancer-associated protein HP14-035.4.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Query Match            10.2%;   Score 321;  DB 8;  Length 628;
Best Local Similarity  23.9%;   Pred. No. 7.6e-12;
RESULT 774
ID   ABO84501 standard; protein; 628 AA.
DE   Human cancer-associated protein HP14-035.2.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Query Match            10.2%;   Score 321;  DB 6;  Length 762;
Best Local Similarity  23.9%;   Pred. No. 9.6e-12;
RESULT 775
ID   ABP70928 standard; protein; 762 AA.
DE   Human LP341 protein.
PN   WO2003029778-A2.
PD   10-APR-2003.
PA   (ELIL ) LILLY & CO ELI.
RESULT 776
ID   ADI36917 standard; protein; 797 AA.
DE   Human LRR protein #12.
PN   US2003222263-A1.
PD   27-NOV-2003.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.

PA   (RAMA/) RAMANATHAN C S.
Query Match            10.2%;   Score 321;  DB 8;  Length 797;
Best Local Similarity  25.5%;   Pred. No. 1e-11;
RESULT 777
ID   ADS98018 standard; protein; 803 AA.
DE   Protein factor discovery related isolated human polypeptide, SEQ ID 282.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
RESULT 778
ID   AAY13349 standard; protein; 660 AA.
DE   Amino acid sequence of protein PRO265.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320;  DB 2;  Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 779
ID   ADC78348 standard; protein; 660 AA.
DE   Human PRO265 protein.
PN   WO200015796-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320;  DB 3;  Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 780
ID   AAB80217 standard; protein; 660 AA.
DE   Human PRO265 protein.
PN   WO200104311-A1.
PD   18-JAN-2001.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320;  DB 4;  Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 781
ID   AAB31208 standard; protein; 660 AA.
DE   Amino acid sequence of human polypeptide PRO265.
PN   WO200077037-A2.
PD   21-DEC-2000.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320;  DB 4;  Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 782
ID   AAU12346 standard; protein; 660 AA.
DE   Human PRO265 polypeptide sequence.
PN   WO200140466-A2.
PD   07-JUN-2001.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320;  DB 4;  Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 783
ID   ABB84839 standard; protein; 660 AA.
DE   Human PRO265 protein sequence SEQ ID NO:46.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320;  DB 5;  Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 784
ID   ABB95445 standard; protein; 660 AA.
DE   Human angiogenesis related protein PRO265 SEQ ID NO: 46.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
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PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match             10.2%;  Score 320;  DB 5;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 785
ID   ABU71595 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US2002146709-A1.
PD   10-OCT-2002.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 786
ID   ABO17790 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 787
ID   ABU71450 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US2002192659-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 788
ID   ABO25179 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003040014-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 789
ID   ABU81044 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003004311-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 790
ID   ABU71896 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2003003530-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 791
ID   ABO01779 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2002197671-A1.
PD   26-DEC-2002.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 792
ID   ABU66744 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003036180-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 793
ID   ABU54352 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2002132240-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 794
ID   ABU67297 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003032063-A1.
PD   13-FEB-2003
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 795
ID   AAO23116 standard; protein; 660 AA.
DE   FLRT2 'human modifier of p53 pathway' protein.
PN   WO2003035833-A2.
PD   01-MAY-2003.
PA   (EXEL-) EXELIXIS INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 796
ID   ABO47367 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003044839-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 797
ID   ABU59825 standard; protein; 660 AA.
DE   Novel secreted and transmembrane protein PRO265.
PN   US2003017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 798
ID   ABO25015 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein (PRO) #175.
PN   US2003036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 799
ID   ABU64504 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2002160374-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 800
ID   ABU72065 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2002177165-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 801
ID   ABU67350 standard; protein; 660 AA.
DE   Human secreted protein PRO265.
PN   US2003023054-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             10.2%;  Score 320;  DB 6;  Length 660;
Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
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RESULT 802
ID   ABU67166 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003032062-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 803
ID   ABO14870 standard; protein; 660 AA.
DE   Human secreted / transmembrane polypeptide PRO265.
PN   US2003036060-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 804
ID   ABU67020 standard; protein; 660 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 350.
PN   US2003032155-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 805
ID   ABU69627 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003017463-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 806
ID   ABU79808 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2003032057-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 807
ID   ABO14809 standard; protein; 660 AA.
DE   Human secreted / transmembrane polypeptide PRO265.
PN   US2003027143-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 808
ID   ADA45869 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 809
ID   ADA76300 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 810
ID   ADB29233 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003092002-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 811
ID   ADA18950 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 812
ID   ADA61573 standard; protein; 660 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 813
ID   ADB19358 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 814
ID   ADB27899 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 815
ID   ADA86378 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 816
ID   ADB15942 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 817
ID   ADA47728 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 818
ID   ADA18089 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003039971-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 819
ID   ABO32761 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2003045693-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity   22.4%; Pred. No. 9.3e-12;

RESULT 820
ID   ADA67523 standard; protein; 660 AA.

DE   Human PRO polypeptide #175.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 821
ID   ADB30530 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 822
ID   ADA85826 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 823
ID   ADA97038 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082705-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 824
ID   ADA79342 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082763-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 825
ID   ADA87481 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087345-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 826
ID   ADB16683 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087349-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 827
ID   ABO34821 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US2003044793-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 828
ID   ADA16064 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003049621-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 829
ID   ADA91775 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.

PN   US2003082694-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 830
ID   ADB14838 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087351-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 831
ID   ADA47287 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003044844-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 832
ID   ADB18799 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003073211-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 833
ID   ADA94014 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077722-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 834
ID   ADB19910 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082691-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 835
ID   ADB13222 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082710-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 836
ID   ABO43323 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003044945-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 837
ID   ADA74476 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003068798-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 6; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 838
ID   ADA42209 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003054401-A1.

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PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 839
ID   ADB24709 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 840
ID   ADA82233 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 841
ID   ADA75196 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 842
ID   ADA85274 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 843
ID   ADA84722 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 844
ID   ABO17499 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 845
ID   ADB29978 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 846
ID   ADA80506 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 847
ID   ADA75748 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082703-A1.
PD   01-MAY-2003.

PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 848
ID   ADA46973 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003073210-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 849
ID   ADB25269 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 850
ID   ADA93445 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 851
ID   ADB26795 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 852
ID   ADB31082 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 853
ID   ADA61010 standard; protein; 660 AA.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 854
ID   ADA24157 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 855
ID   ADA96486 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match           10.2%;   Score 320;  DB 6;   Length 660;
     Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 856
ID   ADA81058 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
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Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 857
ID ADA95934 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 858
ID ADB26243 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 859
ID ADB21728 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 860
ID ADA77507 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 861
ID ADB18247 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 862
ID ADA86930 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 863
ID ADA16488 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 864
ID ADA12917 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 865
ID ADA41785 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 866
ID ADA88033 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 867
ID ADA46421 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 868
ID ADA17132 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 869
ID ADA42635 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 870
ID ADB28451 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 871
ID ADB29003 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 872
ID ADA76955 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 873
ID ADA88585 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 874
ID ADA97590 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;

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RESULT 875
ID ADB27347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 876
ID ADB22280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 877
ID ABO19866 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 878
ID ABO17560 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 879
ID ADA66971 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 880
ID ADB22832 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 881
ID ADB23605 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 882
ID ADA92327 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 883
ID ADB15390 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 884
ID ADB38642 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 885
ID ADB38090 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 886
ID ADB66562 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 887
ID ADB89642 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 888
ID ADB90374 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 889
ID ADB77554 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 890
ID ADB39475 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 891
ID ADB74690 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 892
ID ADB47098 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 893
ID ADB86705 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082697-A1.

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PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 894
ID   ADB77310 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 895
ID   ADB34467 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 896
ID   ADB35571 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 897
ID   ADB33915 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 898
ID   ADB35019 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 899
ID   ADB36123 standard; protein; 660 AA.
DE   Human PRO polypeptide SEQ ID NO 350.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 900
ID   ADB46518 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 901
ID   ADC28336 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003059772-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 902
ID   ADC39536 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003059828-A1.
PD   27-MAR-2003.

PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 903
ID   ADC40050 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003059829-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 904
ID   ADC18878 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003036061-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 905
ID   ADC34174 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003036094-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 906
ID   ADC29229 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003049676-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 907
ID   ADC28760 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003049677-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 908
ID   ADC40645 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003054400-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 909
ID   ADC19302 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003054441-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 910
ID   ADC33750 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003073077-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;    Score 320;   DB 7;   Length 660;
     Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 911
ID   ADC12820 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003073079-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
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Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 912
ID   ADC50391 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003092106-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 913
ID   ADC71938 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003092107-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 914
ID   ADC59917 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003092105-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 915
ID   ADC52924 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein Seq ID350.
PN   US2003087365-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 916
ID   ADC57278 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein Seq ID350.
PN   US2003087366-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 917
ID   ADC60469 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087367-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 918
ID   ADC50944 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087361-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 919
ID   ADC65471 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003087362-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 920
ID   ADC54569 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein Seq ID350.
PN   US2003087363-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;

Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 921
ID   ADC53530 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein Seq ID350.
PN   US2003087364-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 922
ID   ADC59053 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein Seq ID350.
PN   US2003087359-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 923
ID   ADC55931 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein Seq ID350.
PN   US2003087360-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 924
ID   ADC58501 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein Seq ID350.
PN   US2003087346-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 925
ID   ADC12272 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003082541-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 926
ID   ADD03175 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003092104-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 927
ID   ADC90167 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087348-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 928
ID   ADC69586 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194770-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
RESULT 929
ID   ADC48475 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194773-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match           10.2%;    Score 320;  DB 7;  Length 660;
Best Local Similarity    22.4%;    Pred. No. 9.3e-12;
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RESULT 930
ID   ADD10004 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 931
ID   ADD04579 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 932
ID   ADC80535 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 933
ID   ADD11042 standard; protein; 660 AA.
DE   Human secreted and transmembrane protein PRO265.
PN   US2003194774-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 934
ID   ADD10335 standard; protein; 660 AA.
DE   Human secreted/transmembrane PRO polypeptide #23.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 935
ID   ADC47923 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 936
ID   ADD04827 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003104469-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 937
ID   ADC79983 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein PRO265.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 938
ID   ADD11295 standard; protein; 660 AA.
DE   Human secreted/transmembrane PRO polypeptide #23.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 939


ID   ADD09452 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 940
ID   ADD03833 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003104381-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 941
ID   ADD03409 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003108983-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 942
ID   ADD41165 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 943
ID   ADD52304 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 944
ID   ADD53044 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 945
ID   ADD53596 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 946
ID   ADD37088 standard; protein; 660 AA.
DE   Human secreted/transmembrane PRO polypeptide #23.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 947
ID   ADD51752 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660;
     Best Local Similarity   22.4%;
RESULT 948
ID   ADD02551 standard; protein; 660 AA.
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DE  Human PRO polypeptide #175.
PN  US2003203431-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 949
ID  ADD01985 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003203430-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 950
ID  ADD54167 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003203432-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 951
ID  ADD92484 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003199030-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 952
ID  ADD91380 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003199055-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 953
ID  ADE03994 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003194765-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 954
ID  ADE22223 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003199056-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 955
ID  ADD79447 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003203428-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 956
ID  ADE22223 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003203428-A1.
PD  30-OCT-2003.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 957
ID  ADE41983 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
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PN  US2003194772-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 958
ID  ADE17800 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003199023-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 959
ID  ADD91912 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003199053-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 960
ID  ADD33395 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003194767-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 961
ID  ADE33947 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003194791-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 962
ID  ADD79999 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003207417-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 963
ID  ADD93036 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003194768-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 964
ID  ADE19456 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003199025-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 965
ID  ADE34661 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003077583-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match       10.2%;    Score 320;   DB 7;   Length 660;
    Best Local Similarity   22.4%;    Pred. No. 9.3e-12;
RESULT 966
ID  ADE18904 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003199026-A1.
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PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 967
ID   ADE43100 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 968
ID   ADD95889 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199059-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 969
ID   ADE22775 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 970
ID   ADD78893 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 971
ID   ADE32843 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 972
ID   ADE42535 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 973
ID   ADD80551 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 974
ID   ADD89579 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 975
ID   ADE40863 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199031-A1.
PD   23-OCT-2003.

PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 976
ID   ADE04662 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199034-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 977
ID   ADE92791 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194777-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 978
ID   ADG21500 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207355-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 979
ID   ADG23141 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207384-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 980
ID   ADF97476 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207370-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 981
ID   ADG80540 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 982
ID   ADG79988 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 983
ID   ADG63796 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320;  DB 7;  Length 660
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 984
ID   ADH59144 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
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Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 985
ID  ADH55280 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207381-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 986
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADH55832 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207379-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 987
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADI37923 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003054352-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
RESULT 988
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADI65000 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207386-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 989
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADI63499 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207387-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 990
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADH81913 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207388-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 991
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADH81361 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207377-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 992
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADJ26191 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003054349-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
RESULT 993
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADM82530 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003087355-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320; DB 7; Length 660;

Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
RESULT 994
ID  ADN15929 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003087353-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
RESULT 995
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADN16558 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003087385-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
RESULT 996
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADN15377 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003087356-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
RESULT 997
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADN14825 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003087357-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
RESULT 998
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADI64051 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207385-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
RESULT 999
Query Match            10.2%;   Score 320; DB 7; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADC81087 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein, #7.
PN  US2003092115-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
RESULT 1000
Query Match            10.2%;   Score 320; DB 8; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADE79106 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003135025-A1.
PD  17-JUL-2003.
PA  (GETH ) GENENTECH INC.
RESULT 1001
Query Match            10.2%;   Score 320; DB 8; Length 660;
Best Local Similarity  22.4%;   Pred. No. 9.3e-12;
ID  ADD76535 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003100087-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
RESULT.1002
ID  ADD87899 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003092113-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match            10.2%;   Score 320; DB 8; Length 660;
Best Local Similarity  22.4%;
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RESULT 1003
ID   ADD86303 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003203440-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1004
ID   ADE79530 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003130489-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1005
ID   ADE75751 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003211571-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1006
ID   ADE73206 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003129592-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1007
ID   ADE41296 standard; protein; 660 AA.
DE   Human secreted/transmembrane PRO polypeptide #23.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1008
ID   ADE23327 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092108-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1009
ID   ADE23879 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092110-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1010
ID   ADE24522 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003092111-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1011
ID   ADD87347 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1012

ID   ADE89213 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1013
ID   ADE41210 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003104558-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1014
ID   ADE73741 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003148370-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1015
ID   ADE18352 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1016
ID   ADE88661 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1017
ID   ADE99295 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003211576-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1018
ID   ADE94681 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199027-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1019
ID   ADE91092 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1020
ID   ADE95233 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match   10.2%;   Score 320;  DB 8;  Length 660;
  Best Local Similarity  22.4%; Pred. No. 9.3e-12;
RESULT 1021
ID   ADE93343 standard; protein; 660 AA.
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DE   Human PRO polypeptide #175.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1022
ID   ADF34924 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199029-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1023
ID   ADE98414 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003211569-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1024
ID   ADE92239 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1025
ID   ADE90540 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1026
ID   ADE91687 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1027
ID   ADE98841 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003211568-A1.
PD   13-NOV-2003.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1028
ID   ADG40311 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003225253-A1.
PD   04-DEC-2003.
RESULT 1029
ID   ADF73705 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003180312-A1.
PD   25-SEP-2003.

PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1030
ID   ADG02266 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1031
ID   ADG22052 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1032
ID   ADG20122 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1033
ID   ADF98028 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1034
ID   ADG24245 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1035
ID   ADF98599 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1036
ID   ADG03430 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1037
ID   ADF99151 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1038
ID   ADG16736 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   10.2%;   Score 320;   DB 8;   Length 660;
Best Local Similarity   22.4%;
RESULT 1039
ID   ADG05195 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1040
ID   ADG19462 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1041
ID   ADF73281 standard; protein: 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003166051-A1.
PD   04-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1042
ID   ADG13299 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1043
ID   ADG08356 standard; protein: 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1044
ID   ADG15526 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1045
ID   ADF96924 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1046
ID   ADG06109 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1047
ID   ADG23693 standard; protein: 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;

Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1048
ID   ADG03982 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1049
ID   ADG24883 standard; protein: 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207427-A1.
PD   06-NOV-2003
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1050
ID   ADG07180 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1051
ID   ADG07732 standard; protein: 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207356-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1052
ID   ADG55227 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003194778-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1053
ID   ADG60891 standard; protein: 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207390-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1054
ID   ADG61995 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207428-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1055
ID   ADG92124 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003027145-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;
RESULT 1056
ID   ADG82196 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207358-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%;   Score 320;   DB 8;   Length 660;
     Best Local Similarity   22.4%;   Pred. No. 9.3e-12;

RESULT 1057
ID   ADG57435 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207362-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1058
ID   ADG56883 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207364-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1059
ID   ADG55779 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207365-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1060
ID   ADG58539 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207368-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1061
ID   ADG70905 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207420-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1062
ID   ADG92551 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003027146-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1063
ID   ADG57987 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207363-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1064
ID   ADG53571 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207415-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1065
ID   ADG71457 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207421-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1066
ID   ADG81644 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003207805-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1067
ID   ADH30606 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003077723-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1068
ID   ADG63645 standard; protein; 660 AA.
DE   Human secreted/transmembrane polypeptide PRO265.
PN   US2003180796-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1069
ID   ADH11973 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207419-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1070
ID   ADG52395 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1071
ID   ADG54123 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1072
ID   ADG81092 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1073
ID   ADG56331 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1074
ID   ADH12597 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   10.2%; Score 320; DB 8; Length 660;
     Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1075
ID   ADG61443 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.

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PN  US2003207429-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1076
ID  ADH28530 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003022331-A1.
PD  30-JAN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1077
ID  ADG54675 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207367-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1078
ID  ADG59715 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207369-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1079
ID  ADH20340 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2004005553-A1.
PD  08-JAN-2004.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1080
ID  ADH43479 standard; protein; 660 AA.
DE  Human PRO polypeptide #23.
PN  US2003224984-A1.
PD  04-DEC-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1081
ID  ADH07195 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2004006211-A1.
PD  08-JAN-2004.
PA  (DESN/) DESNOYERS L.
PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1082
ID  ADH59740 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003215904-A1.
PD  20-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1083
ID  ADH06768 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2004005665-A1.
PD  08-JAN-2004.
PA  (DESN/) DESNOYERS L.

PA  (GODD/) GODDARD A.
PA  (GODO/) GODOWSKI P J.
PA  (GURN/) GURNEY A L.
PA  (MATH/) MATHER J P.
PA  (WILL/) WILLIAMS P M.
PA  (WOOD/) WOOD W I.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1084
ID  ADI81139 standard; protein; 660 AA.
DE  Human PRO polypeptide #175.
PN  US2003207361-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1085
ID  ADI18510 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003152999-A1.
PD  14-AUG-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1086
ID  ADI65230 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003148419-A1.
PD  07-AUG-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1087
ID  ADI37493 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003096340-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1088
ID  ADG09882 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2004009548-A1.
PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1089
ID  ADH97297 standard; protein; 660 AA.
DE  Human secreted/transmembrane protein, #7.
PN  US2003190610-A1.
PD  09-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1090
ID  ADI15353 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2003207382-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1091
ID  ADG09230 standard; protein; 660 AA.
DE  Novel human secreted and transmembrane protein PRO265.
PN  US2004009547-A1.
PD  15-JAN-2004.
PA  (GETH ) GENENTECH INC.
    Query Match             10.2%;  Score 320;  DB 8;  Length 660;
    Best Local Similarity   22.4%;  Pred. No. 9.3e-12;
RESULT 1092
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ID   ADI14685 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1093
ID   ADH60400 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2004023331-A1.
PD   05-FEB-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1094
ID   ADI18280 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1095
ID   ADJ99457 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003187238-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1096
ID   ADL08650 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003186358-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1097
ID   ADM24995 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2003096233-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1098
ID   ADJ63561 standard; protein; 660 AA.
DE   Novel human secreted and transmembrane protein PRO265.
PN   US2003190611-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1099
ID   ADM29741 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1100
ID   ADJ77456 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004038336-A1.
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PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1101
ID   ADK82824 standard; protein; 660 AA.
DE   Human PRO polypeptide #23.
PN   US2004043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1102
ID   ADJ65578 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1103
ID   ADM27714 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1104
ID   ADM42438 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1105
ID   ADO06063 standard; protein; 660 AA.
DE   Human PRO polypeptide #6.
PN   US6686451-B1.
PD   03-FEB-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1106
ID   ADM28300 standard; protein; 660 AA.
DE   Human PRO polypeptide #175.
PN   US2004077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1107
ID   ADR10915 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2004137561-A1.
PD   15-JUL-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             10.2%;  Score 320; DB 8;  Length 660;
     Best Local Similarity   22.4%;  Pred. No. 9.3e-12;

RESULT 1108
ID   ADR17824 standard; protein; 660 AA.
DE   Human secreted/transmembrane protein, #7.
PN   US2004147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
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PA    (GERB/)  GERBER H.
PA    (GERR/)  GERRITSEN M E.
PA    (GODD/)  GODDARD A.
PA    (GODO/)  GODOWSKI P J.
PA    (GRIM/)  GRIMALDI C J.
PA    (GURN/)  GURNEY A L.
PA    (HILL/)  HILLAN K J.
PA    (KLJA/)  KLJAVIN I J.
PA    (MATH/)  MATHER J P.
PA    (PANJ/)  PAN J.
PA    (PAON/)  PAONI N F.
PA    (ROYM/)  ROY M A.
PA    (STEW/)  STEWART T A.
PA    (TUMA/)  TUMAS D.
PA    (WILL/)  WILLIAMS P M.
PA    (WOOD/)  WOOD W I.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;   .
RESULT 1109
ID    ADI95782 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2003077659-A1.
PD    24-APR-2003.
PA    (GETH )  GENENTECH INC.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1110
ID    ADI96334 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2003207354-A1.
PD    06-NOV-2003.
PA    (GETH )  GENENTECH INC.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1111
ID    ADI65657 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein #7.
PN    US2004185531-A1.
PD    23-SEP-2004.
PA    (ASHK/)  ASHKENAZI A.
PA    (BOTS/)  BOTSTEIN D.
PA    (DESN/)  DESNOYERS L.
PA    (EATO/)  EATON D L.
PA    (FERR/)  FERRARA N.
PA    (FILV/)  FILVAROFF E.
PA    (FONG/)  FONG S.
PA    (GAOW/)  GAO W.
PA    (GERB/)  GERBER H.
PA    (GERR/)  GERRITSEN M E.
PA    (GODD/)  GODDARD A.
PA    (GODO/)  GODOWSKI P J.
PA    (GRIM/)  GRIMALDI C J.
PA    (GURN/)  GURNEY A L.
PA    (HILL/)  HILLAN K J.
PA    (KLJA/)  KLJAVIN I J.
PA    (MATH/)  MATHER J P.
PA    (PANJ/)  PAN J.
PA    (PAON/)  PAONI N F.
PA    (ROYM/)  ROY M A.
PA    (STEW/)  STEWART T A.
PA    (TUMA/)  TUMAS D.
PA    (WILL/)  WILLIAMS P M.
PA    (WOOD/)  WOOD W I.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;

RESULT 1113
ID    ADS32286 standard; protein; 660 AA.
DE    Novel human secreted and transmembrane protein PRO265.
PN    US2004203125-A1.
PD    14-OCT-2004.
PA    (GETH )  GENENTECH INC.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1114
ID    ADT03270 standard; protein; 660 AA.
DE    Human PRO polypeptide #175.
PN    US2004214269-A1.
PD    28-OCT-2004.
PA    (GETH )  GENENTECH INC.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1115
ID    ADT03500 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2003152922-A1.
PD    14-AUG-2003.
PA    (GETH )  GENENTECH INC.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1116
ID    ADU06386 standard; protein; 660 AA.
DE    Novel bronchial cancer-associated human protein SeqID610.
PN    DE10316701-A1.
PD    04-NOV-2004.
PA    (HINZ/)  HINZMANN B.
PA    (HERM/)  HERMANN K.
PA    (CAST/)  HEIDEN CASTANOS-VELEZ E.
Query Match           10.2%;    Score 320;    DB 8;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1117
ID    AD203321 standard; protein; 660 AA.
DE    Human secreted/transmembrane PRO265 protein.
PN    US2005074837-A1.
PD    07-APR-2005.
PA    (GETH )  GENENTECH INC.
Query Match           10.2%;    Score 320;    DB 9;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1118
ID    AEA37738 standard; protein; 660 AA.
DE    Human secreted/transmembrane protein, #7.
PN    US2005112725-A1.
PD    26-MAY-2005.
PA    (GETH )  GENENTECH INC.
Query Match           10.2%;    Score 320;    DB 9;   Length 660;
Best Local Similarity  22.4%;    Pred. No. 9.3e-12;
RESULT 1119
ID    AEB14067 standard; protein; 660 AA.
DE    Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN    US2005153396-A1.
PD    14-JUL-2005.
PA    (BAKE/)  BAKER K P.
PA    (BERE/)  BERESINI M.
PA    (DEFO/)  DEFORGE L.
PA    (DESN/)  DESNOYERS L.
PA    (FILV/)  FILVAROFF E.
PA    (GAOW/)  GAO W.
PA    (GERR/)  GERRITSEN M E.
PA    (GODD/)  GODDARD A.
PA    (GODO/)  GODOWSKI P J.
PA    (GURN/)  GURNEY A L.
PA    (SHER/)  SHERWOOD S.
PA    (SMIT/)  SMITH V.
PA    (STEW/)  STEWART T A.
PA    (TUMA/)  TUMAS D.
PA    (WATA/)  WATANABE C K.
PA    (WOOD/)  WOOD W I.
PA    (ZHAN/)  ZHANG Z.
Query Match           10.2%;    Score 320;    DB 9;   Length 660;
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        Best Local Similarity  22.4%;  Pred. No. 9.3e-12;
RESULT 1120
ID   ADT77808 standard; protein; 452 AA.
DE   Chimeric Nogo receptor polypeptide.
PN   WO2004090103-A2.
PD   21-OCT-2004.
PA   (UYRP ) UNIV ROCHESTER.
        Query Match  10.2%;  Score 318.5;  DB 8;  Length 452;
        Best Local Similarity  27.3%;  Pred. No. 7.5e-12;
RESULT 1121
ID   ADT77802 standard; protein; 452 AA.
DE   Chimeric Nogo receptor polypeptide.
PN   WO2004090103-A2.
PD   21-OCT-2004.
PA   (UYRP ) UNIV ROCHESTER.
        Query Match  10.2%;  Score 318.5;  DB 8;  Length 452;
        Best Local Similarity  27.8%;  Pred. No. 7.5e-12;
RESULT 1122
ID   AAE13006 standard; protein; 713 AA.
DE   Human leucine-rich repeat (LRR) family member protein.
PN   WO200175105-A2.
PD   11-OCT-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
        Query Match  10.1%;  Score 317.5;  DB 4;  Length 713;
        Best Local Similarity  23.1%;  Pred. No. 1.5e-11;
RESULT 1123
ID   AAU91335 standard; protein; 713 AA.
DE   Human novel secreted protein LP223(a).
PN   WO200214358-A2.
PD   21-FEB-2002.
PA   (ELIL ) LILLY & CO ELI.
        Query Match  10.1%;  Score 316.5;  DB 5;  Length 713;
        Best Local Similarity  23.1%;  Pred. No. 1.7e-11;
RESULT 1124
ID   ABG97991 standard; protein; 713 AA.
DE   Human nervous system leucine rich repeat protein (HLRRNS1) #2.
PN   WO200274959-A2.
PD   26-SEP-2002.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
        Query Match  10.1%;  Score 316.5;  DB 5;  Length 713;
        Best Local Similarity  23.1%;  Pred. No. 1.7e-11;
RESULT 1125
ID   ABU52381 standard; protein; 713 AA.
DE   Human GPCR related protein NOV31a.
PN   WO200279398-A2.
PD   10-OCT-2002.
PA   (CURA-) CURAGEN CORP.
        Query Match  10.1%;  Score 316.5;  DB 6;  Length 713;
        Best Local Similarity  23.1%;  Pred. No. 1.7e-11;
RESULT 1126
ID   ADT77796 standard; protein; 474 AA.
DE   Chimeric Nogo receptor polypeptide.
PN   WO2004090103-A2.
PD   21-OCT-2004.
PA   (UYRP ) UNIV ROCHESTER.
        Query Match  10.0%;  Score 314.5;  DB 8;  Length 474;
        Best Local Similarity  27.8%;  Pred. No. 1.4e-11;
RESULT 1127
ID   AAU91341 standard; protein; 656 AA.
DE   Human novel secreted protein LP223(b).
PN   WO200214358-A2.
PD   21-FEB-2002.
PA   (ELIL ) LILLY & CO ELI.
        Query Match  10.0%;  Score 313.5;  DB 5;  Length 656;
        Best Local Similarity  23.6%;  Pred. No. 2.4e-11;
RESULT 1128
ID   ADL24097 standard; protein; 713 AA.
DE   Human NOVX polypeptide #71.
PN   US2004002120-A1.
PD   01-JAN-2004.
PA   (KEKU/) KEKUDA R.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (PATT/) PATTURAJAN M.
PA   (BURG/) BURGESS C E.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (GORM/) GORMAN L.
PA   (MALY/) MALYANKAR U M.
PA   (BOLD/) BOLDOG F L.
PA   (GUOX/) GUO X.
PA   (SHEN/) SHENOY S G.
PA   (PADI/) PADIGARU M.
PA   (TAUP/) TAUPIER R J.
PA   (MILL/) MILLER C E.
PA   (CASM/) CASMAN S J.
PA   (PENA/) PENA C E A.
PA   (GANG/) GANGOLLI E A.
PA   (GUSE/) GUSEV V Y.
PA   (SMIT/) SMITHSON G.
PA   (ZERH/) ZERHUSEN B D.
PA   (GERL/) GERLACH V.
PA   (POCH/) POCHART P F.
PA   (FERN/) FERNANDES E R.
PA   (SHIM/) SHIMKETS R A.
PA   (RAST/) RASTELLI L.
PA   (SPAD/) SPADERNA S K.
PA   (LARO/) LAROCHELLE W J.
PA   (ZHON/) ZHONG M.
PA   (KHRA/) KHRAMTSOV N V.
PA   (VOSS/) VOSS E Z.
PA   (HERR/) HERRMANN J L.
        Query Match  10.0%;  Score 313.5;  DB 8;  Length 713;
        Best Local Similarity  23.1%;  Pred. No. 2.6e-11;
RESULT 1129
ID   AAE09437 standard; protein; 592 AA.
DE   Human sbgTango79a protein.
PN   WO200160850-A1.
PD   23-AUG-2001.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
        Query Match  10.0%;  Score 312;  DB 4;  Length 592;
        Best Local Similarity  25.9%;  Pred. No. 2.6e-11;
RESULT 1130
ID   AAE25351 standard; protein; 592 AA.
DE   Human LP polypeptide, LP243.
PN   WO200248361-A2.
PD   20-JUN-2002.
PA   (ELIL ) LILLY & CO ELI.
        Query Match  10.0%;  Score 312;  DB 5;  Length 592;
        Best Local Similarity  25.9%;  Pred. No. 2.6e-11;
RESULT 1131
ID   AAU91329 standard; protein; 592 AA.
DE   Human novel secreted protein LP243(b).
PN   WO200214358-A2.
PD   21-FEB-2002.
PA   (ELIL ) LILLY & CO ELI.
        Query Match  10.0%;  Score 312;  DB 5;  Length 592;
        Best Local Similarity  25.9%;  Pred. No. 2.6e-11;
RESULT 1132
ID   ABP60996 standard; protein; 592 AA.
DE   Novel human protein. SEQ ID 83.
PN   WO200250105-A1.
PD   27-JUN-2002.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
        Query Match  10.0%;  Score 312;  DB 5;  Length 592;
        Best Local Similarity  25.9%;  Pred. No. 2.6e-11;
RESULT 1133
ID   AAU79167 standard; protein; 592 AA.
DE   Human leucine-rich repeat proteins-like protein NOV4.
PN   WO200214368-A2.
PD   21-FEB-2002.
PA   (CURA-) CURAGEN CORP.
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Query Match         10.0%;  Score 312; DB 5; Length 592;
Best Local Similarity 25.9%;  Pred. No. 2.6e-11;
RESULT 1134
ID   ABG74693 standard; protein; 592 AA.
DE   Human CGDD protein 6803363CD1 SEQ ID 19.
PN   WO2003014322-A2.
PD   20-FEB-2003.
PA   (INCY-) INCYTE GENOMICS INC.

Query Match         10.0%;  Score 312; DB 6; Length 592;
Best Local Similarity 25.9%;  Pred. No. 2.6e-11;
RESULT 1135
ID   ADE03417 standard; protein; 592 AA.
DE   Human immunoglobulin superfamily member BGS-2.
PN   US2003195163-A1.
PD   16-OCT-2003.
PA   (WUSS/) WU S.
PA   (KRYS/) KRYSTEK S R.
PA   (LEEL/) LEE L.
PA   (FEDE/) FEDER J N.
PA   (CHEN/) CHENG J D.

Query Match         10.0%;  Score 312; DB 7; Length 592;
Best Local Similarity 25.9%;  Pred. No. 2.6e-11;
RESULT 1136
ID   ADU02709 standard; protein; 592 AA.
DE   Novel human polypeptide seqid 1176.
PN   WO2004093804-A2.
PD   04-NOV-2004.
PA   (FIVE) FIVE PRIME THERAPEUTICS INC.

Query Match         10.0%;  Score 312; DB 8; Length 608;
Best Local Similarity 25.9%;  Pred. No. 2.6e-11;
RESULT 1137
ID   ABG61770 standard; protein; 608 AA.
DE   Novel leucine-rich protein.
PN   WO200229058-A2.
PD   11-APR-2002.
PA   (CURA-) CURAGEN CORP.

Query Match         10.0%;  Score 312; DB 5; Length 634;
Best Local Similarity 25.9%;  Pred. No. 2.7e-11;
RESULT 1138
ID   ABG97967 standard; protein; 634 AA.
DE   Human nervous system leucine rich repeat protein (HLRRNS1) #1.
PN   WO200274959-A2.
PD   26-SEP-2002.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.

Query Match          9.9%;  Score 311; DB 5; Length 634;
Best Local Similarity 24.1%;  Pred. No. 3.3e-11;
RESULT 1139
ID   ABR55628 standard; protein; 420 AA.
DE   Amino acid sequence of rat Nogo-66 receptor homologue NgRH1.
PN   WO2003035833-A2.
PD   01-MAY-2003.
PA   (NOVS ) NOVARTIS AG.

Query Match          9.9%;  Score 310.5; DB 6; Length 420;
Best Local Similarity 29.8%;  Pred. No. 2.2e-11;
RESULT 1140
ID   ADT77788 standard; protein; 420 AA.
DE   Rat Nogo receptor 2 polypeptide.
PN   WO2003035587-A1.
PD   01-MAY-2003.
PA   (NOVS ) NOVARTIS PHARMA GMBH.

Query Match          9.9%;  Score 310.5; DB 6; Length 420;
Best Local Similarity 29.8%;  Pred. No. 2.2e-11;
RESULT 1141
ID   AAO23115 standard; protein; 674 AA.
DE   FLRT1 'human modifier of p53 pathway' protein.
PN   WO200110902-A2.
PD   21-OCT-2004.
PA   (UYRP ) UNIV ROCHESTER.

Query Match          9.9%;  Score 310.5; DB 6; Length 674;
Best Local Similarity 21.5%;  Pred. No. 3.8e-11;
RESULT 1142
ID   ADH17606 standard; protein; 674 AA.
DE   Human NOV19a protein - SEQ ID 296.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.

Query Match          9.9%;  Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%;  Pred. No. 3.8e-11;
RESULT 1143
ID   ADH17628 standard; protein; 674 AA.
DE   Human NOV19l protein - SEQ ID 318.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.

Query Match          9.9%;  Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%;  Pred. No. 3.8e-11;
RESULT 1144
ID   ADH17630 standard; protein; 674 AA.
DE   Human NOV19m protein - SEQ ID 320.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.

Query Match          9.9%;  Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%;  Pred. No. 3.8e-11;
RESULT 1145
ID   ADH17634 standard; protein; 674 AA.
DE   Human NOV19o protein - SEQ ID 324.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.

Query Match          9.9%;  Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%;  Pred. No. 3.8e-11;
RESULT 1146
ID   ADH17632 standard; protein; 674 AA.
DE   Human NOV19n protein - SEQ ID 322.
PN   WO2003093432-A2.
PD   13-NOV-2003.
PA   (CURA-) CURAGEN CORP.

Query Match          9.9%;  Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%;  Pred. No. 3.8e-11;
RESULT 1147
ID   ABO27346 standard; protein; 585 AA.
DE   Human secreted/transmembrane polypeptide PRO1865.
PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match          9.9%;  Score 309; DB 6; Length 585;
Best Local Similarity 22.3%;  Pred. No. 4e-11;
RESULT 1148
ID   ABO34232 standard; protein; 585 AA.
DE   Human secreted/transmembrane polypeptide PRO 1865.
PN   US2003060601-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          9.9%;  Score 309; DB 6; Length 585;
Best Local Similarity 22.3%;  Pred. No. 4e-11;
RESULT 1149
ID   AAU29215 standard; protein; 649 AA.
DE   Human PRO polypeptide sequence #192.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH ) GENENTECH INC.

Query Match          9.9%;  Score 309; DB 4; Length 649;
Best Local Similarity 22.3%;  Pred. No. 4.6e-11;
RESULT 1150
ID   AAB70533 standard; protein; 649 AA.
DE   Human PRO3 protein sequence SEQ ID NO:6.
PN   WO200110902-A2.
PD   15-FEB-2001.
PA   (CURA-) CURAGEN CORP.

Query Match          9.9%;  Score 309; DB 4; Length 649;
Best Local Similarity 22.3%;  Pred. No. 4.6e-11;
RESULT 1151
ID   AAB87591 standard; protein; 649 AA.
DE   Human PRO1865.
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PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1152
ID ABG95916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US200119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1153
ID ABB84953 standard; protein; 649 AA.
DE Human PRO1865 protein sequence SEQ ID NO:274.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1154
ID ABP70109 standard; protein; 649 AA.
DE Human NOV27a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1155
ID ABB95559 standard; protein; 649 AA.
DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1156
ID ABU58591 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US200302272-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1157
ID ABU08139 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US200303127-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1158
ID ABU84454 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US200303112-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1159
ID ABR66328 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US200307278-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1160
ID ABR65718 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US200303159-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1161
ID ABU99658 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US200304070-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1162
ID ABU82897 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US200303113-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1163
ID ABU90018 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US200303167-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1164
ID ABR68267 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US200307264-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1165
ID ABU96120 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US200306144-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1166
ID ABU92751 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US200306149-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1167
ID ABO08828 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US200304923-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1168
ID ABO02880 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US200304062-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1169
ID ABR75034 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

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PN  US2003040056-A1.
PD  27-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1170
ID  ABR94796 standard; protein; 649 AA.
DE  Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN  US2003044926-A1.
PD  06-MAR-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1171
ID  ABU85769 standard; protein; 649 AA.
DE  Human PRO polypeptide #192.
PN  US2003036140-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1172
ID  ABU98929 standard; protein; 649 AA.
DE  Novel human secreted and transmembrane protein PRO1865.
PN  US2003013153-A1.
PD  16-JAN-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1173
ID  ABU98144 standard; protein; 649 AA.
DE  Novel human secreted and transmembrane protein PRO1865.
PN  US2003017554-A1.
PD  23-JAN-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1174
ID  ABU91850 standard; protein; 649 AA.
DE  Novel human secreted and transmembrane protein PRO1865.
PN  US2003027277-A1.
PD  06-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1175
ID  ABU89543 standard; protein; 649 AA.
DE  Human PRO protein #192.
PN  US2003036141-A1.
PD  20-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1176
ID  ABU86384 standard; protein; 649 AA.
DE  Human secreted/transmembrane protein (PRO) #192.
PN  US2003036146-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1177
ID  ABU67597 standard; protein; 649 AA.
DE  Human secreted/transmembrane protein (PRO) #192.
PN  US2003036162-A1.
PD  20-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1178
ID  ABU80625 standard; protein; 649 AA.
DE  Human PRO protein #192.
PN  US2003036137-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1179
ID  ABU90941 standard; protein; 649 AA.
DE  Novel human secreted and transmembrane protein PRO1865.
PN  US2003018173-A1.
PD  23-JAN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1180
ID  ABO34000 standard; protein; 649 AA.
DE  Human secreted/transmembrane protein PRO1865.
PN  US2003009013-A1.
PD  09-JAN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1181
ID  ABR99543 standard; protein; 649 AA.
DE  Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN  US2003040063-A1.
PD  27-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1182
ID  ABR98933 standard; protein; 649 AA.
DE  Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN  US2003040064-A1.
PD  27-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1183
ID  ABO16456 standard; protein; 649 AA.
DE  Human secreted/transmembrane protein (PRO) #192.
PN  US2003027267-A1.
PD  06-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1184
ID  ABR92356 standard; protein; 649 AA.
DE  Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN  US2003036160-A1.
PD  20-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1185
ID  ABO18997 standard; protein; 649 AA.
DE  Human secreted/transmembrane protein (PRO) #192.
PN  US2003044925-A1.
PD  06-MAR-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1186
ID  ABR78418 standard; protein; 649 AA.
DE  Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN  US2003054474-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1187
ID  ABU72017 standard; protein; 649 AA.
DE  Novel human secreted and transmembrane protein PRO1865.
PN  US2003018183-A1.
PD  23-JAN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1188
ID  ABU85154 standard; protein; 649 AA.
DE  Novel human secreted and transmembrane protein PRO1865.
PN  US2003032114-A1.
PD  13-FEB-2003.
    Query Match             9.9%;  Score 309;  DB 6;  Length 649;
    Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1189
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ID    AB00293 standard; protein; 649 AA.
DE    Novel human secreted and transmembrane protein PRO1865.
PN    US2003032101-A1.
PD    13-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1190
ID    AB011625 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003036124-A1.
PD    20-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1191
ID    AB002270 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003040054-A1.
PD    27-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1192
ID    ABU88844 standard; protein; 649 AA.
DE    Novel human secreted and transmembrane protein PRO1865.
PN    US2003036133-A1.
PD    20-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1193
ID    ABU83539 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003036134-A1.
PD    20-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1194
ID    AB006340 standard; protein; 649 AA.
DE    Novel human secreted and transmembrane protein PRO1865.
PN    US2003022294-A1.
PD    30-JAN-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1195
ID    ABR59376 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003027275-A1.
PD    06-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1196
ID    AB009438 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003027324-A1.
PD    06-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1197
ID    AB019302 standard; protein; 649 AA.
DE    Novel human secreted and transmembrane protein PRO1865.
PN    US2003036118-A1.
PD    20-FEB-2003.
PA    (GETH ) GENENTECH INC.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1198
ID    AB011320 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003036123-A1.
PD    20-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1199
ID    ABR66938 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN    US2003036148-A1.
PD    20-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1200
ID    AB016151 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003040060-A1.
PD    27-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1201
ID    AB013857 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003044916-A1.
PD    06-MAR-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1202
ID    ABU71571 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865.
PN    US2003013855-A1.
PD    16-JAN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1203
ID    ABU65760 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein, SEQ ID 384.
PN    US2003036156-A1.
PD    20-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1204
ID    AB007608 standard; protein; 649 AA.
DE    Human PRO polypeptide #192.
PN    US2003032117-A1.
PD    13-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1205
ID    AB003795 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003036128-A1.
PD    20-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1206
ID    ABR67243 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003022266-A1.
PD    06-FEB-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1207
ID    AB015846 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003054483-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1208
ID    ABU56127 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein, PRO1865.
PN    US2003022298-A1.
PD    30-JAN-2003.
      Query Match    9.9%;    Score 309; DB 6; Length 649;
      Best Local Similarity  22.3%;  Pred. No. 4.6e-11;
RESULT 1209
ID    ABU72352 standard; protein; 649 AA.
DE    Human PRO polypeptide #66.
PN    US2002182638-A1.
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PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1210
ID   ABU65455 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032102-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1211
ID   ABU95400 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036117-A1.
PD   20-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1212
ID   ABU71303 standard; protein; 649 AA.
DE   Human PRO1865 protein.
PN   US2003036143-A1.
PD   20-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1213
ID   ABO07913 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032130-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1214
ID   ABR70154 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032138-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1215
ID   ABR69487 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036132-A1.
PD   20-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1216
ID   ABO01628 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003008353-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1217
ID   ABU81430 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003017542-A1.
PD   23-JAN-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1218
ID   ABR60227 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032137-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1219
ID   ABU91025 standard; protein; 649 AA.
DE   Human PRO polypeptide #66.
PN   US2003018168-A1.

PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1220
ID   ABR67962 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027269-A1.
PD   06-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1221
ID   ABR65350 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027268-A1.
PD   06-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1222
ID   ABR68572 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027274-A1.
PD   06-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1223
ID   ABR71984 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1224
ID   ABU85464 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003022295-A1.
PD   30-JAN-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1225
ID   ABU89154 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003022297-A1.
PD   30-JAN-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1226
ID   ABU83234 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032105-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1227
ID   ABU95090 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032123-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1228
ID   ABU90638 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032108-A1.
PD   13-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1229
ID   ABU84149 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032111-A1.
PD   13-FEB-2003.

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        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1230
ID   ABU93800 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1231
ID   ABR65045 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027263-A1.
PD   06-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1232
ID   ABR68877 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027271-A1.
PD   06-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1233
ID   ABO06693 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036125-A1.
PD   20-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1234
ID   ABR99238 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040068-A1.
PD   27-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1235
ID   ABU57122 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003027280-A1.
PD   06-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1236
ID   ABU86074 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003022300-A1.
PD   30-JAN-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1237
ID   ABU82361 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036136-A1.
PD   20-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1238
ID   ABU87372 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003036138-A1.
PD   20-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1239
ID   ABU83844 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032109-A1.
PD   13-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1240
ID   ABO08218 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003040066-A1.
PD   27-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1241
ID   ABU92541 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein PRO1865.
PN   US2003045684-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1242
ID   ABU81929 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032104-A1.
PD   13-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1243
ID   ABU66093 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036157-A1.
PD   20-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1244
ID   ABU81211 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865.
PN   US2003027212-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1245
ID   ABR59922 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032120-A1.
PD   13-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1246
ID   ABU94110 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036155-A1.
PD   20-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1247
ID   ABU99963 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003022296-A1.
PD   30-JAN-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1248
ID   ABR66633 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1249
ID   ABR91051 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040058-A1.
PD   27-FEB-2003.
        Query Match              9.9%;   Score 309;  DB 6;  Length 649;
        Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
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RESULT 1250
ID   ABO53325 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003027986-A1.
PA   (GETH) GENENTECH INC.
PD   06-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1251
ID   ABU94478 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003017540-A1.
PD   23-JAN-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1252
ID   ABU79360 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032106-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1253
ID   ABU86689 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032129-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1254
ID   ABU86994 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032131-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1255
ID   ABU94783 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032103-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1256
ID   ABO04710 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032107-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1257
ID   ABR70459 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032139-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1258
ID   ABU98624 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003022301-A1.
PD   30-JAN-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1259
ID   ABR66023 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036165-A1.
PA   (GETH) GENENTECH INC.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1260

RESULT 1250
ID   ABR64740 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027262-A1.
PD   06-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1261
ID   ABU79665 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032110-A1.
PD   13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1262
ID   ABU93056 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036142-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1263
ID   ABU96015 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003036145-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1264
ID   ABU91235 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036154-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1265
ID   ABU90328 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036153-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1266
ID   ABO09743 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044931-A1.
PD   06-MAR-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1267
ID   ABO11015 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036150-A1.
PD   20-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1268
ID   ABR71069 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040069-A1.
PD   27-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1269
ID   ABU98328 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1270
ID   ABU87677 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.

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PN   US2003022293-A1.
PD   30-JAN-2003.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1271
ID   ABU91545 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032128-A1.
PD   13-FEB-2003.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1272
ID   ABU89333 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1273
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABU84759 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032116-A1.
PD   13-FEB-2003.
RESULT 1274
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABR69849 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032122-A1.
PD   13-FEB-2003.
RESULT 1275
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABU80226 standard; protein; 649 AA.
DE   Human PRO protein #192.
PN   US2003036139-A1.
PD   20-FEB-2003.
RESULT 1276
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABU82540 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2002183494-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
RESULT 1277
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABU93495 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003017541-A1.
PD   23-JAN-2003.
RESULT 1278
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABO10048 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003017543-A1.
PD   23-JAN-2003.
RESULT 1279
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABO09133 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036152-A1.
PD   20-FEB-2003.
RESULT 1280
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
ID   ABU96504 standard; protein; 649 AA.
DE   Human PRO polypeptide #66.
PN   US2003027993-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1281
ID   ABU10701 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein #192.
PN   US2002127584-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1282
ID   ABU72174 standard; protein; 649 AA.
DE   Human PRO polypeptide #66.
PN   US2003023042-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1283
ID   ABU95710 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003032115-A1.
PD   13-FEB-2003.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1284
ID   ABU96919 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003032140-A1.
PD   13-FEB-2003.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1285
ID   ABR70764 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1286
ID   ABO05115 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003008352-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1287
ID   ABO08523 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044922-A1.
PD   06-MAR-2003.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1288
ID   ABO05730 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032118-A1.
PD   13-FEB-2003.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1289
ID   ABR74119 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036135-A1.
PD   20-FEB-2003.
       Query Match             9.9%;     Score 309; DB 6;    Length 649;
       Best Local Similarity  22.3%;     Pred. No. 4.6e-11;
RESULT 1290
ID   ABR95711 standard; protein; 649 AA.
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DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1291
ID   ABR81008 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1292
ID   ABR81313 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1293
ID   ABM01009 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049769-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1294
ID   ABR88611 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1295
ID   ABM77432 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054479-A1.
PD   20-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1296
ID   AB028916 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1297
ID   AB031661 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1298
ID   ABM08078 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1299
ID   AB040558 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1300
ID   AB035983 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068701-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1301
ID   AB044122 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068755-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1302
ID   ADA78136 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003073180-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1303
ID   ABM24917 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104539-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1304
ID   AB003185 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036131-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1305
ID   ABR90441 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040075-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1306
ID   ABM17355 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054459-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1307
ID   ABR95101 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040930-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
RESULT 1308
ID   ABR95406 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             9.9%;  Score 309;  DB 6;  Length 649;
     Best Local Similarity   22.3%;  Pred. No. 4.6e-11;
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RESULT 1309
ID   ADB17189 standard; protein; 649 AA.
DE   Human transmembrane PRO polypeptide (SeqID 132).
PN   US2003050462-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1310
ID   ABO21644 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1311
ID   ABR97908 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1312
ID   ABR87696 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1313
ID   ABM77737 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064440-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1314
ID   ABM27967 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064440-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1315
ID   ABM06248 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068704-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1316
ID   ABM03754 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1317
ID   ABM35205 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1318
ID   ABM26442 standard; protein; 649 AA.

DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1319
ID   ABO48224 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1320
ID   ABR92966 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1321
ID   ABO24727 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1322
ID   ABM11738 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1323
ID   ABM02839 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1324
ID   ABM16135 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1325
ID   ABO27696 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1326
ID   ABM29187 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003066721-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%;   Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1327
ID   ABM07163 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1328
ID ABM21257 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1329
ID ABM09603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1330
ID ABO41473 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1331
ID ABO36288 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1332
ID ABO43817 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1333
ID ABM76517 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1334
ID ABM76213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1335
ID ABM25832 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1336
ID ABM26137 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;

Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1337
ID ABO3490 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1338
ID ABO02575 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1339
ID ABO44304 standard; protein; 649 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1340
ID ABR90746 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1341
ID ABR73814 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1342
ID ABO17066 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1343
ID ABR94491 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1344
ID ABR75998 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1345
ID ABR71374 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1346
ID A2R93271 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064465-A1.
PD 03-APR-2003.

PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1347
ID   ABR93576 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1348
ID   ABR88001 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1349
ID   ABO28001 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1350
ID   ABO30136 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1351
ID   ABO33345 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1352
ID   ABM05033 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1353
ID   ABM08993 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1354
ID   ABO36593 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1355
ID   ABO35678 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1356
ID   ABO39643 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068776-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1357
ID   ABM10518 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003069407-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1358
ID   ABM12043 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1359
ID   ABO52189 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1360
ID   ABO52494 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1361
ID   ADA19994 standard; protein; 649 AA.
DE   Novel human secreted and transmembrane protein PRO1865.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1362
ID   ABO23812 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032134-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1363
ID   ADB17377 standard; protein; 649 AA.
DE   Human transmembrane PRO polypeptide (SeqID 132).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1364
ID   ABR97298 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;

RESULT 1365
ID   ABR87086 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1366
ID   ABM11128 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1367
ID   ABM28272 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1368
ID   ABO32271 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1369
ID   ABM15398 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1370
ID   ABM06553 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1371
ID   ABM04364 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1372
ID   ABM22477 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1373
ID   ABM07773 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1374
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ID   ABO40863 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1375
ID   ABM35510 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1376
ID   ABM33273 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003087374-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1377
ID   ABO52799 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1378
ID   ABO50359 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1379
ID   ABU99353 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040055-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1380
ID   ABO04405 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003036164-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1381
ID   ABO06035 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040074-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1382
ID   ABM18575 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1383
ID   ABR97603 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.

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        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1384
ID   ABR80703 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049940-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1385
ID   ABM01314 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1386
ID   ABR88916 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073169-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1387
ID   ABM13568 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1388
ID   ABM20952 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1389
ID   ABO42083 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1390
ID   ABO42693 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1391
ID   ABM10213 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064448-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1392
ID   ABO38728 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068773-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;


RESULT 1393
ID   ABM32968 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1394
ID   ABM22782 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003087373-A1.
PD   08-MAY-2003.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1395
ID   ABM74993 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003096353-A1.
PD   22-MAY-2003.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1396
ID   ADA79928 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003073173-A1.
PD   17-APR-2003.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1397
ID   ABR96383 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054458-A1.
PD   20-MAR-2003.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1398
ID   ABM02534 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1399
ID   ABR86476 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049758-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1400
ID   ABR86781 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1401
ID   ABM16745 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match          9.9%;  Score 309;  DB 6;  Length 649;
        Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1402
ID   ABM29797 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064456-A1.
PD   03-APR-2003.
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PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1403
ID    ABO29221 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003068693-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1404
ID    ABM24002 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003068735-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1405
ID    ABM23392 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003068753-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1406
ID    ABM22172 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003068742-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1407
ID    ABO37813 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003068756-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1408
ID    ABM28577 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003082715-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1409
ID    ABM28882 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003082716-A1.
PD    01-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1410
ID    ABM65526 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003068737-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1411
ID    ABM75908 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003104547-A1.
PD    05-JUN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;

RESULT 1412
ID    ABM34188 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003096359-A1.
PD    22-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1413
ID    ABM34493 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003100061-A1.
PD    29-MAY-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1414
ID    ABO20424 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003032125-A1.
PD    13-FEB-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1415
ID    ABO21339 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003054454-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1416
ID    ABO22254 standard; protein; 649 AA.
DE    Human secreted/transmembrane protein (PRO) #192.
PN    US2003054477-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1417
ID    ADA20166 standard; protein; 649 AA.
DE    Novel human secreted and transmembrane protein PRO1865.
PN    US2003055222-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1418
ID    ABR96688 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003054460-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1419
ID    ABR85866 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003049753-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1420
ID    ABR99848 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN    US2003049763-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             9.9%;    Score 309;    DB 6;    Length 649;
      Best Local Similarity   22.3%;   Pred. No. 4.6e-11;
RESULT 1421
ID    ABM00399 standard; protein; 649 AA.
DE    Human secreted polypeptide PRO1865, SEQ ID NO:384.
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PN US2003073172-A1.
PD 17-APR-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1422
ID ABM00704 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1423
ID ABO29831 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1424
ID ABM23697 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1425
ID ABM29492 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1426
ID ABO38423 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1427
ID ABO45723 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1428
ID ABM20647 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1429
ID ADA81655 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1430
ID ABO16761 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;

Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1431
ID ABO18387 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1432
ID ABO22814 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1433
ID ABO23119 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1434
ID ABR92661 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1435
ID ABR81618 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1436
ID ABM78042 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1437
ID ABR89831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1438
ID ABM26747 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1439
ID ABM13873 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   9.9%; Score 309; DB 6; Length 649;
Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1440
ID ABO28611 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064460-A1.

PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1441
ID   ABO30441 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1442
ID   ABM07468 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1443
ID   ABM04059 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1444
ID   ABO37203 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1445
ID   ABO41778 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068729-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1446
ID   ABO35373 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1447
ID   ABM25222 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104540-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1448
ID   ABO47614 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1449
ID   ABO47919 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1450
ID   ABO48529 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1451
ID   ABO51579 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1452
ID   ABO51884 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049767-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1453
ID   ABO50664 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049779-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1454
ID   ABR79788 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040059-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1455
ID   ABM17050 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040078-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1456
ID   ABO18082 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003044918-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1457
ID   ABO21034 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032133-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1458
ID   ABR96993 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1459
ID   ABM12348 standard; protein; 649 AA.

DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064445-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1460
ID   ABM16440 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064449-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1461
ID   ABM24307 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064441-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1462
ID   ABM14788 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068696-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1463
ID   ABM04669 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068712-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1464
ID   ABM06858 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068730-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1465
ID   ABM09298 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003073174-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1466
ID   ABO39338 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068775-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1467
ID   ABM75603 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104545-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1468
ID   ABM25527 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104541-A1.
PD   05-JUN-2003.

     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1469
ID   ABM20037 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003104554-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1470
ID   ABO46943 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049762-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1471
ID   ABO47248 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049765-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1472
ID   ADA83453 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1473
ID   ABR71679 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032133-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1474
ID   ABR72289 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003032136-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1475
ID   ABR98628 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003036129-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1476
ID   ABO06998 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003040053-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1477
ID   ABR84951 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003040057-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1478
ID   ABR73509 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054467-A1.

PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1479
ID   ABR76603 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003044932-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1480
ID   ABR73204 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003027270-A1.
PD   06-FEB-2003.
     Query Match   9.9%; Score 309; DB 6; Length 649
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1481
ID   ABM18270 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003054469-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
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RESULT 1482
ID   ABO20729 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003032126-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
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RESULT 1483
ID   ABO22472 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
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PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
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RESULT 1484
ID   ABO25777 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003054466-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1485
ID   ABR94186 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003059879-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1486
ID   ABR80093 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003049738-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1487
ID   ABM11433 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003064469-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1488

ID   ABO33040 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003064453-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1489
ID   ABO30746 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064466-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1490
ID   ABO31051 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003064468-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1491
ID   ABM27357 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068760-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1492
ID   ABM30102 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068769-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1493
ID   ABM05638 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003045700-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1494
ID   ABM15703 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068698-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1495
ID   ABM08688 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068759-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1496
ID   ABO42388 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   9.9%; Score 309; DB 6; Length 649;
     Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1497
ID   ABO38118 standard; protein; 649 AA.

DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003068765-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match   9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1498
ID   AB046028 standard; protein; 649 AA.
DE   Human PRO polypeptide #192.
PN   US2003049754-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match   9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1499
ID   ABM66831 standard; protein; 649 AA.
DE   Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN   US2003068668-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match   9.9%; Score 309; DB 6; Length 649;
  Best Local Similarity   22.3%; Pred. No. 4.6e-11;
RESULT 1500
ID   ADB20496 standard; protein; 649 AA.
DE   Human secreted/transmembrane protein (PRO) #192.
PN   US2003082767-A1.
PD   01-MAY-2003.
  Query Match   9.9%; Score 309; DB 6; Length 649;
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                GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January  5, 2006, 13:53:04 ; Search time 167 Seconds
                                      (without alignments)
                                      1496.179 Million cell updates/sec

Perfect score: 3135
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Searched:      1867569 seqs, 41782 9326 residues

Total number of hits satisfying chosen parameters:    1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
3	3135	100.0	598	3	US-09-944-457-69	Sequence 69, Appl
70	3135	100.0	598	4	US-10-219-065-104	Sequence 104, App
121	3135	100.0	598	4	US-10-429-667-69	Sequence 69, Appl
126	3135	100.0	598	4	US-10-677-471-69	Sequence 69, Appl
127	3135	100.0	598	5	US-10-677-669-69	Sequence 69, Appl
129	3135	100.0	598	5	US-10-735-014-69	Sequence 69, Appl
130	3135	100.0	598	5	US-10-854-947-69	Sequence 69, Appl
131	3135	100.0	598	5	US-10-858-993-69	Sequence 69, Appl
133	3135	100.0	598	5	US-10-901-400-69	Sequence 69, Appl
134	3135	100.0	598	5	US-10-858-981-69	Sequence 69, Appl
135	3135	100.0	598	5	US-10-899-671-69	Sequence 69, Appl
136	3135	100.0	598	5	US-10-943-353-69	Sequence 69, Appl
138	3083.5	98.4	673	3	US-09-782-980-59	Sequence 59, Appl
164	3083.5	98.4	673	4	US-09-997-428-52	Sequence 52, Appl
265	3083.5	98.4	673	4	US-10-063-742-16	Sequence 16, Appl
358	3083.5	98.4	673	4	US-10-806-018-59	Sequence 59, Appl
359	3083.5	98.4	673	5	US-10-972-317-16	Sequence 16, Appl
360	3083.5	98.2	673	5	US-10-950-374-52	Sequence 52, Appl
361	3078.5	98.2	676	4	US-10-029-386-33083	Sequence 33083, A
362	2935	93.6	672	4	US-10-050-704-99	Sequence 99, Appl
363	2935	93.6	672	4	US-10-798-512-99	Sequence 99, Appl
364	2935	93.6	723	4	US-10-050-704-186	Sequence 186, App
365	2935	93.6	723	5	US-10-798-512-186	Sequence 186, App
366	2490	79.4	673	3	US-09-782-980-68	Sequence 68, Appl
367	2490	79.4	673	4	US-10-806-018-68	Sequence 68, Appl
368	2484	79.2	673	4	US-10-487-421-10	Sequence 10, Appl
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372	360.5	11.5	647	4	US-10-093-463-188	Sequence 188, App
373	357.5	11.4	778	4	US-10-093-463-192	Sequence 192, App
374	339	10.8	566	4	US-10-093-463-190	Sequence 190, App
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SUMMARIES

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3	330	10.5	653	7	US-11-135-855-25	Sequence 25, Appl
4	321	10.2	628	7	US-11-147-047-45	Sequence 45, Appl
6	312	10.0	592	7	US-11-135-855-24	Sequence 24, Appl
7	309	9.9	649	7	US-11-102-240-132	Sequence 132, Appl
11	282.5	9.0	745	7	US-11-135-855-37	Sequence 37, Appl
12	282	9.0	626	7	US-11-010-748A-1	Sequence 1, Appl
15	249.5	8.0	479	7	US-11-147-047-44	Sequence 44, Appl
17	237.5	7.6	344	7	US-11-055-163-6	Sequence 6, Appl
18	237	7.6	349	7	US-11-147-047-47	Sequence 47, Appl
19	229	7.3	581	7	US-11-089-872-1	Sequence 1, Appli
20	227	7.2	310	7	US-11-055-163-7	Sequence 7, Appli
21	227	7.2	771	7	US-11-147-047-34	Sequence 34, Appl
22	225.5	7.2	766	7	US-11-135-855-24	Sequence 24, Appl
25	214.5	6.8	716	7	US-11-147-047-52	Sequence 52, Appl
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27	214	6.8	2828	7	US-11-186-284-49	Sequence 49, Appli
28	212	6.8	310	7	US-11-055-163-9	Sequence 9, Appli
29	212	6.8	344	7	US-11-055-163-8	Sequence 8, Appli
31	211	6.7	513	7	US-11-102-240-124	Sequence 124, App
32	209.5	6.7	606	6	US-10-624-932-18	Sequence 18, Appl
34	205.5	6.6	533	7	US-11-147-047-33	Sequence 33, Appl
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36	200.5	6.4	845	7	US-11-147-047-46	Sequence 46, Appl
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67	147.5	4.7	2108	6	US-10-995-561-989	Sequence 989, App
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84	136	4.3	737	6	US-10-055-877-156	Sequence 156, App
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233	95	3.0	614	7	US-11-155-492-107	Sequence 107, App
234	95	3.0	1767	6	US-10-995-561-911	Sequence 911, App
235	95	3.0	1767	6	US-10-995-561-914	Sequence 914, App
236	95	3.0	1806	6	US-10-995-561-912	Sequence 912, App
237	95	3.0	1806	6	US-10-995-561-915	Sequence 915, App
238	95	3.0	1818	6	US-10-995-561-910	Sequence 910, App
239	95	3.0	1818	6	US-10-995-561-913	Sequence 913, App
240	95	3.0	2098	6	US-10-055-877-253	Sequence 253, App
241	94.5	3.0	1259	6	US-10-995-561-625	Sequence 625, App
242	94.5	3.0	1286	6	US-10-995-561-628	Sequence 628, App
243	94.5	3.0	1315	6	US-10-995-561-630	Sequence 630, App
244	94.5	3.0	1341	6	US-10-995-561-621	Sequence 621, App
245	94.5	3.0	2296	6	US-10-995-561-633	Sequence 633, App
246	94.5	3.0	2355	6	US-10-995-561-623	Sequence 623, App
247	94.5	3.0	2355	6	US-10-995-561-627	Sequence 627, App
248	94.5	3.0	2384	6	US-10-821-234-1545	Sequence 1545, Ap
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253	94	3.0	863	7	US-11-114-906-32	Sequence 32, Appl
254	94	3.0	876	7	US-11-114-906-30	Sequence 30, Appl
255	94	3.0	951	7	US-11-114-906-36	Sequence 36, Appl
256	94	3.0	957	7	US-11-114-906-34	Sequence 34, Appl
257	94	3.0	976	7	US-11-114-906-28	Sequence 28, Appl
258	94	3.0	982	7	US-11-114-906-26	Sequence 26, Appl
259	94	3.0	2011	7	US-11-080-991-56	Sequence 56, Appl
260	93.5	3.0	418	7	US-11-196-919-2	Sequence 2, Appli
261	93.5	3.0	461	7	US-11-132-285-6	Sequence 6, Appli
262	93.5	3.0	461	7	US-11-182-946-4	Sequence 4, Appli
263	93.5	3.0	614	7	US-11-015-546A-20	Sequence 20, Appl
264	93.5	3.0	833	7	US-11-076-187-5	Sequence 5, Appli
265	93	3.0	378	6	US-11-087-177-41	Sequence 41, Appl
266	93	3.0	833	6	US-10-667-295-102	Sequence 102, App
267	93	3.0	839	6	US-10-667-295-101	Sequence 101, App
268	93	3.0	891	7	US-11-205-109-18	Sequence 18, Appl
269	92.5	3.0	419	7	US-11-113-202-4	Sequence 4, Appli
270	92	2.9	471	6	US-10-858-730-125	Sequence 125, App
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272	92	2.9	998	6	US-10-510-524-1	Sequence 1, Appli

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291	2.9	90	537	US-10-504-364-7	7	Sequence 7, Appli
292	2.9	90	818	US-11-037-243-111	7	Sequence 111, App
293	2.9	90	837	US-11-127-877-74	7	Sequence 74, Appl
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309	2.8	87.5	1686	US-11-109-157A-1	7	Sequence 1, Appli
310	2.8	87.5	3063	US-11-186-284-26	6	Sequence 26, Appl
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312	2.8	87.5	188	US-10-945-853-1	6	Sequence 1, Appli
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325	2.8	87.5	1053	US-11-052-554A-151	6	Sequence 151, App
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335	2.8	87	438	US-10-821-234-1051	6	Sequence 1051, Ap
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338	2.8	87	615	US-10-995-561-940	6	Sequence 940, App
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345	2.8	87	2801	US-11-124-368A-305	7	Sequence 305, App
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347	2.8	87	3256	US-11-124-368A-304	7	Sequence 304, App
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353	2.7	86	381	US-10-821-234-1342	6	Sequence 1342, Ap
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355	2.7	86	574	US-11-102-240-164	7	Sequence 164, App
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357	2.7	86	665	US-11-124-368A-289	6	Sequence 289, App
358	2.7	86	847	US-10-995-561-634	6	Sequence 634, App
359	2.7	86	899	US-11-124-368A-290	6	Sequence 290, App
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365	2.7	85.5	720	US-11-102-240-38	7	Sequence 38, Appl
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369	2.7	85.5	923	US-11-192-219-4	7	Sequence 4, Appli
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371	2.7	85.5	1174	US-10-995-561-697	6	Sequence 697, App
372	2.7	85.5	1250	US-11-137-465-62	7	Sequence 62, Appl
373	2.7	85.5	2764	US-10-995-561-691	6	Sequence 691, App
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375	2.7	85.5	2919	US-10-821-234-1133	6	Sequence 1133, Ap
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377	2.7	85	536	US-10-641-678-70	6	Sequence 70, Appl
378	2.7	85	595	US-11-182-946-9	7	Sequence 9, Appli
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383	2.7	84.5	335	US-11-136-619-30	7	Sequence 30, Appl
384	2.7	84.5	351	US-11-136-619-14	7	Sequence 14, Appl
386	2.7	84.5	379	US-11-136-619-2	7	Sequence 2, Appli
387	2.7	84.5	379	US-11-136-619-22	7	Sequence 22, Appl
388	2.7	84.5	379	US-11-136-619-23	7	Sequence 23, Appl
389	2.7	84.5	740	US-11-137-465-61	7	Sequence 61, Appl
390	2.7	84.5	1254	US-10-528-031-47	7	Sequence 47, Appl
391	2.7	84	1493	US-11-004-057-21	7	Sequence 21, Appl
392	2.7	84	302	US-10-467-657-4028	6	Sequence 4028, Ap
393	2.7	84	868	US-10-821-234-1082	6	Sequence 1082, Ap
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395	2.7	84	965	US-11-147-047-51	7	Sequence 51, Appl
396	2.7	83.5	567	US-11-000-463-400	6	Sequence 400, App
397	2.7	83.5	711	US-10-821-234-1017	6	Sequence 1017, Ap
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402	2.6	83	232	US-11-128-059-66	7	Sequence 66, Appl
403	2.6	83	313	US-10-485-517-123	6	Sequence 123, App
404	2.6	83	313	US-10-485-517-293	6	Sequence 293, App
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406	2.6	83	549	US-11-096-070-6	7	Sequence 6, Appli
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408	2.6	83	744	US-11-186-284-39	6	Sequence 39, Appl
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410	2.6	83	931	US-11-128-059-86	7	Sequence 86, Appl
411	2.6	83	1194	US-11-000-463-249	6	Sequence 249, App
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414	2.6	83	1327	US-11-128-059-84	7	Sequence 84, Appl
415	2.6	83	1416	US-11-128-059-4	7	Sequence 4, Appli
416	2.6	83	1637	US-10-821-234-1204	6	Sequence 1204, Ap
417	2.6	83	2086	US-11-128-059-82	7	Sequence 82, Appl
418	2.6	83	2313	US-11-128-059-80	7	Sequence 80, Appl
419	2.6	83	2358	US-11-128-059-74	7	Sequence 74, Appl
420	2.6	83	2458	US-11-128-059-94	7	Sequence 94, Appl
421	2.6	83	2551	US-11-128-059-96	7	Sequence 96, Appl
422	2.6	82.5	235	US-11-126-126-16	7	Sequence 16, Appl

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426	82.5	2.6	463	7	US-11-000-463-872	Sequence 872, App
428	82.5	2.6	510	6	US-10-641-678-43	Sequence 43, Appl
429	82.5	2.6	511	6	US-10-641-678-42	Sequence 42, Appl
430	82.5	2.6	526	6	US-10-641-678-46	Sequence 46, Appl
431	82.5	2.6	615	6	US-10-982-545-14	Sequence 14, Appl
432	82.5	2.6	948	6	US-10-485-517-131	Sequence 131, App
433	82.5	2.6	965	6	US-11-113-424-2	Sequence 2, Appli
434	82.5	2.6	984	6	US-10-995-561-629	Sequence 629, App
435	82.5	2.6	1366	6	US-11-000-463-1431	Sequence 1431, Ap
436	82.5	2.6	1366	6	US-10-821-234-31	Sequence 31, Appl
437	82.5	2.6	1400	6	US-10-821-234-1045	Sequence 1045, Ap
438	82.5	2.6	1433	7	US-11-094-519A-40	Sequence 40, Appl
439	82.5	2.6	4384	6	US-10-821-234-1120	Sequence 1120, Ap
440	82	2.6	255	6	US-10-467-657-2044	Sequence 2044, Ap
441	82	2.6	470	6	US-10-967-527A-30	Sequence 30, Appl
442	82	2.6	470	7	US-10-979-821-14	Sequence 14, Appl
443	82	2.6	470	7	US-11-114-922-14	Sequence 14, Appl
444	82	2.6	550	6	US-10-504-364-8	Sequence 8, Appli
445	82	2.6	550	6	US-10-504-364-9	Sequence 9, Appli
446	82	2.6	672	7	US-11-000-463-455	Sequence 455, Appl
447	82	2.6	685	7	US-10-661-966-3	Sequence 3, Appl
448	82	2.6	744	6	US-11-186-284-37	Sequence 37, Appl
449	82	2.6	765	6	US-10-661-966-10	Sequence 10, Appl
450	82	2.6	765	6	US-10-661-966-15	Sequence 15, Appl
451	82	2.6	768	6	US-10-995-561-956	Sequence 956, App
452	82	2.6	783	6	US-10-661-966-2	Sequence 2, Appl
453	82	2.6	830	6	US-10-995-561-957	Sequence 957, App
454	82	2.6	830	6	US-10-995-561-958	Sequence 958, App
455	82	2.6	909	7	US-11-186-284-2	Sequence 2, Appl
456	82	2.6	912	6	US-10-964-313-12	Sequence 12, Appl
457	82	2.6	913	7	US-10-821-234-1040	Sequence 1040, Ap
458	82	2.6	1062	6	US-10-821-234-1079	Sequence 1079, App
460	82	2.6	1302	6	US-11-004-057-6	Sequence 6, Appl
461	82	2.6	1463	6	US-10-971-982-3	Sequence 3, Appli
462	82	2.6	1874	6	US-10-821-234-1182	Sequence 1182, Ap
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477	81	2.6	2107	6	US-10-995-561-827	Sequence 827, App
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479	81	2.6	3116	6	US-10-995-561-826	Sequence 826, App
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482	80.5	2.6	523	7	US-10-641-678-45	Sequence 45, Appl
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484	80.5	2.6	637	6	US-10-821-234-961	Sequence 961, Appl
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486	80.5	2.6	1126	7	US-11-110-480-9	Sequence 9, Appli
487	80.5	2.6	1126	7	US-11-110-480-16	Sequence 16, Appl
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489	80.5	2.6	1126	7	US-11-110-480-37	Sequence 37, Appl
490	80.5	2.6	1126	7	US-11-110-480-47	Sequence 47, Appl
491	80.5	2.6	1126	7	US-11-110-480-59	Sequence 59, Appl
492	80.5	2.6	1126	7	US-11-110-480-82	Sequence 82, Appl
493	80.5	2.6	1126	7	US-11-110-480-88	Sequence 88, Appl
494	80.5	2.6	1615	7	US-11-110-480-80	Sequence 80, Appl
495	80	2.6	156	7	US-10-401-386B-44	Sequence 44, Appl
496	80	2.6	426	7	US-11-055-822-450	Sequence 450, Appl
497	80	2.6	451	7	US-11-102-240-82	Sequence 82, Appl
498	80	2.6	512	7	US-11-108-172-1093	Sequence 1093, Ap
499	80	2.6	589	6	US-10-821-234-1687	Sequence 1687, Ap
500	80	2.6	757	7	US-11-052-554A-378	Sequence 378, App
501	80	2.6	901	7	US-11-082-389-430	Sequence 430, App
502	80	2.6	1051	6	US-11-205-109-13	Sequence 13, Appl
503	80	2.6	1255	6	US-10-770-726-62	Sequence 62, Appl
504	80	2.6	1255	7	US-11-113-202-10	Sequence 10, Appl
505	80	2.6	4374	7	US-11-128-572-2	Sequence 2, Appli
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1073	2.1	65.5	730	US-10-821-234-1019	6	Sequence 1019, Ap
1074	2.1	65.5	742	US-10-658-986-2	6	Sequence 2, Appli
1075	2.1	65.5	755	US-11-067-121-6	7	Sequence 6, Appli
1076	2.1	65.5	777	US-10-658-986-4	6	Sequence 4, Appli
1077	2.1	65.5	844	US-10-763-712A-48	6	Sequence 48, Appl
1078	2.1	65.5	904	US-10-967-648A-14	6	Sequence 14, Appl
1079	2.1	65.5	1091	US-11-000-463-348	7	Sequence 348, App
1080	2.1	65.5	1213	US-11-039-398-14	7	Sequence 14, Appl
1081	2.1	65.5	1308	US-11-113-202-16	7	Sequence 16, Appl
1082	2.1	65.5	2096	US-10-995-561-606	6	Sequence 606, App
1083	2.1	65.5	2351	US-10-995-561-608	6	Sequence 608, App
1084	2.1	65	176	US-11-052-554A-197	7	Sequence 197, App
1085	2.1	65	215	US-10-374-954-7	6	Sequence 7, Appli
1086	2.1	65	277	US-11-132-285-3	7	Sequence 3, Appli
1087	2.1	65	277	US-11-182-946-12	7	Sequence 12, Appl
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1091	2.1	65	425	US-11-197-721-8	7	Sequence 8, Appli
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1105	2.1	65	579	US-10-623-155-449	6	Sequence 449, App
1106	2.1	65	579	US-10-623-155-480	6	Sequence 480, App
1107	2.1	65	579	US-10-623-155-484	6	Sequence 484, App
1108	2.1	65	580	US-10-995-561-987	6	Sequence 987, App
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1119	2.1	65	1124	US-11-195-197-9	7	Sequence 9, Appli
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1122	2.1	65	2523	US-11-052-554A-143	7	Sequence 143, App
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1166	2.0	64	190	US-10-063-343-30	6	Sequence 30, Appl
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1176	64	2.0	291	6	US-10-467-657-4148	Sequence 4148, Ap
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1178	64	2.0	337	6	US-10-821-234-1004	Sequence 1004, Ap
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1184	64	2.0	475	7	US-11-061-869-15	Sequence 15, Appl
1185	64	2.0	478	6	US-10-821-234-915	Sequence 915, App
1186	64	2.0	519	7	US-11-099-691-10	Sequence 10, Appl
1187	64	2.0	547	6	US-10-770-726-87	Sequence 87, Appl
1188	64	2.0	611	7	US-11-082-389-436	Sequence 436, App
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1202	63.5	2.0	955	7	US-11-052-554A-179	Sequence 179, App
1203	63.5	2.0	995	7	US-11-113-424-62	Sequence 62, Appl
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1225	63.5	2.0	305	7	US-11-087-177-7	Sequence 7, Appli
1226	63.5	2.0	312	7	US-11-055-822-868	Sequence 868, App
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1230	63.5	2.0	345	7	US-11-210-316-14	Sequence 14, Appl
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1232	63.5	2.0	371	6	US-10-995-561-572	Sequence 572, App
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1273	63	2.0	386	7	US-11-060-029-13	Sequence 13, Appl
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1279	63	2.0	505	6	US-10-063-343-38	Sequence 38, Appl
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1298	62.5	2.0	185	6	US-10-967-527A-32	Sequence 32, Appl
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1312	62.5	2.0	506	6	US-10-967-527A-22	Sequence 22, Appl
1313	62.5	2.0	510	7	US-11-074-176-184	Sequence 184, App
1314	62.5	2.0	577	6	US-10-510-386-240	Sequence 240, App
1315	62.5	2.0	595	6	US-10-884-730-381	Sequence 381, App
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1328	62.5	2.0	747	7	US-10-995-561-840	Sequence 840, App
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1370	62	2.0	487	6	US-11-113-424-56	Sequence 56, Appl
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